

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 19:34:58 ; Search time 1997 Seconds
(without alignments)

7132.829 Million cell updates/sec

Title: US-10-071-370A-3

Perfect score: 477

Sequence: 1 atgtcgccatgaagctgtt.....ctgaggaacccacctgtga 477

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:**

2: em_esthma:**

3: em_estma:**

4: em_estma:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_htc:**

9: gb_estl:**

10: gb_est2:**

11: gb_htc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pln:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_mam:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rod:**

26: em_gss_phg:**

27: em_gss_vrl:**

28: gb_gss1:**

29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
C 1	449.8	94.3	616 13	BU759674
2	419.4	87.9	421 14	CE797697
3	419.4	87.9	829 10	BE569697
4	419.4	87.9	863 14	CF616127

5	419.4	87.9	1583	11	AK042891	Mus muscu
6	412.8	86.5	936	12	BI905649	AK088943
7	407.4	85.4	1579	11	AK088943	Mus muscu
8	405.2	84.9	932	14	CB204450	AGENCOURT
9	405.2	84.9	933	13	BQ936933	AGENCOURT
10	402.4	84.4	744	12	BI663772	AGENCOURT
11	364.6	76.4	455	9	AI272466	uk06c06.y
12	361.8	75.8	759	12	BI685632	603309146
13	361.2	75.7	489	12	BI790853	1409h10.y
14	361.2	75.7	958	14	CF582990	AGENCOURT
15	358.8	75.2	908	12	BI108026	602902409
16	343.6	72.0	794	12	BI852987	603739807
17	341.2	71.5	733	12	BG923923	602824355
18	337	70.6	709	10	AW914155	EST345459
19	332.4	69.7	874	10	BE570632	601329939
20	331.6	69.5	724	12	BI692908	603344629
21	331.4	69.5	458	14	CB739080	AMGNNUC:M
22	323.4	67.8	942	14	CA976301	AGENCOURT
23	317.8	66.6	806	12	BI648112	603278429
24	313.6	65.7	785	12	BG976319	602846588
25	311.8	65.4	665	12	BI525252	602924679
26	297.8	62.4	669	12	BI653120	603300663
27	284.2	59.6	657	12	BG920099	602821273
28	282.2	59.2	482	29	AY410378	Mus muscu
29	278.8	58.4	837	12	BI662663	603286057
30	271.2	56.9	673	10	BF608215	MY1_00109
31	258.8	54.3	678	13	BQ109005	imageqc 8
32	238.4	50.0	958	9	AL543693	AL543693
33	234.6	49.2	617	10	BE533260	601234582
34	230.2	48.3	513	29	AY410376	Homo sapi
35	230.2	48.3	513	29	AY410377	Pan trogl
36	230.2	48.3	1009	11	CNSL119B	human ful
37	230.2	48.3	1031	13	BQ070531	AGENCOURT
38	230.2	48.3	1153	9	AL552106	AL552106
39	230.2	48.3	1201	9	AL543185	AL543185
40	230.2	48.3	1201	9	AL547463	AL547463
41	229.8	48.2	986	9	AL552344	AL552344
42	229.8	48.2	1035	9	AL546005	AL546005
43	229.8	48.2	1201	9	AL540600	AL540600
44	228.6	47.9	1201	13	BX459214	BX459214
45	227.2	47.6	939	13	BU150305	AGENCOURT

ALIGNMENTS

RESULT 1	BU759674/c	616 bp	linear	EST 10-OCT-2002
LOCUS	BU759674	616 bp	linear	EST 10-OCT-2002
DEFINITION	UI-R-PF0-cpf-c-16-0-UI.sl	UI-R-PF0	Rattus norvegicus	cdna clone
ACCESSION	BU759674	UI-R-PF0-cpf-c-16-0-UI 3', mRNA sequence.		
VERSION	BU759674.1	GI:23723459		
KEYWORDS	EST.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
REFERENCE	1 (bases 1 to 616)			
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.			
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery			
JOURNAL	Genome Res. 6 (9), 791-806 (1996)			
MEDLINE	97044477			
PubMed	8889548			
COMMENT	Contact: Soares, MB			
	Coordinated Laboratory for Computational Genomics			
	University of Iowa			
	375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA			
	Tel: 319 335 8250			
	Fax: 319 335 9565			
	Email: bento-soares@uiowa.edu			

Tissue Procurement: Jeff Stevens, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: DISTRIBUTION: Researchers may obtain clones
 from Research Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-26, >POLY A#simple_repeat (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source
 Location/Qualifiers
 1..616
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="UI-R-FPO-cpf-c-16-0-UI"
 /tissue_type="Mixed tissues"
 /dev_stage="Adult"
 /lab_host="DHI0B (Life Technologies) (71 phage resistant)"
 /lab_lib="UI-R-FPO"
 /note="Vector: pT7T3-Pac (Pharmacia) with a modified
 polylinker; Site 1: EcoR I; Site 2: Not I; UI-R-FPO is a
 subtracted cDNA library containing the following
 tissue(s): Normal cartilage and SR-JWS Tumor line. The
 subtraction was made according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. The
 oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for these libraries are: CTAATGGACG,
 CATTCTGTGA.
 TAG TISSUE=cartilage
 TAG LIB=UI-R-FPO
 TAG_SEQ=CTAATGGACG"

ORIGIN
 Query Match 94.3%; Score 449.8; DB 13; Length 616;
 Best Local Similarity 99.0%; Pred. No. 1.1e-113;
 Matches 473; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
 QY 1 ATGCTGCCATGAAGCTGTTCACTTCTTTCAGTCTCTAGCTGGTGGCTGGAC 60
 Db 558 ATGCTGCCATGAAGCTGTTCACTTCTTTCAGTCTCTAGCTGGTGGCTGGAC 499
 QY 61 T-CCAGGGGGCCCTGTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGCTTTCAA 119
 Db 498 TCCCAGGGGGCCCTGTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGCTTTCAA 439
 QY 120 TGAAGTGGGGCCGAGCTACTCCGGCCCAATGGAGAGCTGGTGTACATTCAGATGA 179
 Db 438 TGAAGTGGGGCCGAGCTACTCCGGCCCAATGGAGAGCTGGTGTACATTCAGATGA 379
 QY 180 ACACCTTAATGAAGTGTCTCATATATTCACTGCTCGTCTATGTCCTTCTGAGTGGCTAG 239
 Db 378 ACACCTTAATGAAGTGTCTCATATATTCACTGCTCGTCTATGTCCTTCTGAGTGGCTAG 319
 QY 240 TGGCTGTGTGTGACGAGGGTCTGCACTGTGTGGCGCTAAAGACAGCCAACTACTAT 299
 Db 318 TGGCTGTGTGTGACGAGGGTCTGCACTGTGTGGCGCTAAAGACAGCCAACTACTAT 259
 QY 300 GCAGATCTTAAGATTCGCCCAATCCGGATCCACATTCCTAGTGGAGATGACATCTC 359
 Db 259 GCAGATCTTAAGATTCGCCCAATCCGGATCCACATTCCTAGTGGAGATGACATCTC 199
 QY 360 TCAGATGTACTCTGCGAATGAGGCTTATTCGAGAGAGCAACAAGGCGAAGAGGAGAA 419
 Db 198 TCAGATGTACTCTGCGAATGAGGCTTATTCGAGAGAGCAACAAGGCGAAGAGGAGAA 139
 QY 420 AACCAAGGGGAGAGGAAGCAAGCAAAACCCACAGACTGAGGAACCCCACTGTGA 477
 Db 138 AACCAAGGGGAGAGGAGC-AAGCAAAACCCACAGACTGAGGAACCCCACTGTGA 82

RESULT 2
 CB797697
 LOCUS
 DEFINITION
 AMGNNUC.MRPE4-00164-G5-A mrpe4 (10380) Rattus norvegicus cDNA clone
 mrpe4-00164-g5 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelesostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 421)
 Amgen EST Program
 Amgen Rat EST Program
 Unpublished (2003)
 CONTACT: Dan Fitzpatrick
 Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00164 row: 9 column: 5.
 Location/Qualifiers
 1..421
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="mrpe4-00164-g5"
 /tissue_type="placenta embryo"
 /clone_lib="mrpe4 (10380)"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI;
 placenta embryo day 17"

ORIGIN
 Query Match 87.9%; Score 413.4; DB 14; Length 421;
 Best Local Similarity 99.8%; Pred. No. 2.5e-105;
 Matches 420; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GCTGGCCATGAAGCTGTTCACTTGTCTTTCAGAGTCTCTAGCTGGTGGCTGGACATC 62
 Db 1 GCTGGCCATGAAGCTGTTCACTTGTCTTTCAGAGTCTCTAGCTGGTGGCTGGACATC 60
 QY 63 CCAGGGGGCCCTGTCTGCTGGGAAACAACCTCAACAGAAATGGAAGTGGCTTTCAATGA 122
 Db 61 CCAGGGGGCCCTGTCTGCTGGGAAACAACCTCAACAGAAATGGAAGTGGCTTTCAATGA 120
 QY 123 AGTGTGGGGCCGAGCTACTCCGGCCCAATGGAGAGCTGGTGTACATTCGAGATGAAC 182
 Db 121 AGTGTGGGGCCGAGCTACTCCGGCCCAATGGAGAGCTGGTGTACATTCGAGATGAAC 180
 QY 183 CCTTAATGAAGTGTCTCATATATTCACTGCTCGTCTATGTCCTTCTGAGTGGCTAGTGG 242
 Db 181 CCTTAATGAAGTGTCTCATATATTCACTGCTCGTCTATGTCCTTCTGAGTGGCTAGTGG 240
 QY 243 CTGCTGTGTGTGACGAGGGTCTGCATCTGTGGCGCTAAAGACAGCCAACTACTATGA 302
 Db 241 CTGCTGTGTGTGACGAGGGTCTGCATCTGTGGCGCTAAAGACAGCCAACTACTATGA 300
 QY 303 GATCTTAAGATTCGCCCAATCCGGATCCACATTCCTAGTGGAGATGACATTCCTCA 362
 Db 301 GATCTTAAGATTCGCCCAATCCGGATCCACATTCCTAGTGGAGATGACATTCCTCA 360
 QY 363 GGATGTACTCTCGAATGAGGCTTATTCGAGAGAGCAACAAGGCGAAGAGGAGAAAC 422
 Db 361 GGATGTACTCTCGAATGAGGCTTATTCGAGAGAGCAACAAGGCGAAGAGGAGAAAC 420
 QY 423 C 423
 Db 421 C 421

RESULT 3
 BS569697

LOCUS B569697 829 bp mRNA linear EST 15-AUG-2000
 DEFINITION 60131496F1 NCI_QGAP_Mam6 Mus musculus cDNA clone IMAGE:3709294 5', mRNA sequence.
 ACCESSION B569697
 VERSION B569697.1 GI:9813521
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 829)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Cloning distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LAM929 row: o column: 23
 High quality sequence stop: 721.
 FEATURES
 source
 1. 829
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:3709294"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI_QGAP Mam6"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
 ORIGIN
 Query Match 87.9%; Score 419.4; DB 10; Length 829;
 Best Local Similarity 92.5%; Pred. No. 3.2e-105;
 Matches 441; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 Qy 1 ATGCTGCCCATGAGCTGTTCACTTGCTTCTTGAGTCCCTAGCTGGTGGCTGGCTGCAC 60
 Db 14 ATGCTGGTCATGAAGCTGTTCACTTGCTTCTTACAGGTCCCTAGCTGGTGGCTGGCTGCAT 73
 Qy 61 TCCAGAGGGGCCCTGCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTTCAAT 120
 Db 74 TCCAGAGGGGCCCTGCTGCTGGGAACAACCTCAACAGAGTGGAGTGGTCCCTTTCAAC 133
 Qy 121 GAAGTGTGGGGCCGAGCTACTCGCGCCAAATGAGAGAGCTGGTGTACATTGCAGATGAA 180
 Db 134 GAAGTGTGGGGTCGAGCTACTGTCGGCCCAATGAGAGAGCTGGTGTACATCTTGGATGAA 193
 Qy 181 CACCTAATGAAGTGTCTCATATATTAGTCCGTCATGTGCTTCTGAGTCGCTGTAGT 240
 Db 194 TACCCTGATGAGGTGTCCTACATATTACGTCCGTCCTGTGCTTCTGAGTCGCTGTAGT 253
 Qy 241 GGCTGCTGTGTGAGAGGGTCTGCACGTGTGGCGCTTAAAGACAGCCAAACATCACTATG 300
 Db 254 GGCTGCTGTGTGATGAAGGTCTGCACGTGTGGCGCTTAAAGACAGCCAAACATCACTATG 313
 Qy 301 CAGATCTTTAAAGATTCCCGCCCAATCGGATCCATTCTCTACGTGGAGATGACATTTCTCT 360
 Db 314 CAGATCTTGAAGATTCCCGCCCAATCGGATCCATTCTCTATGTGGAGATGACATTTCTCT 373
 Qy 361 CAGGATGTACTCTGCGAATGAGGCGCTATTCTGGAGACGACAAAGGCGAAGAGGAGAA 420

Db 374 CAGATGTGCTGTGTAATCGACACTTATTCTGGAGACGACAAAGGCGAGAAAGAGGAAA 433
 Qy 421 ACCAAGGGGAGAGGAGCAAGCAAAACCCACAGACTGAGGAAACCCACCTGTGA 477
 Db 434 ACCAAGGGGAGAGGAGGAGGAGTAGAACTTCACAGACTGAGGAAACCCACCTGTGA 490
 RESULT 4
 CF616127 863 bp mRNA linear EST 01-OCT-2003
 LOCUS CF616127
 DEFINITION AGENCOURT 15765547 NIH MGC 203 Mus musculus cDNA clone
 IMAGE:30522779 5', mRNA sequence.
 ACCESSION CF616127
 VERSION CF616127.1 GI:37232101
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 863)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Naryan Bhat
 CDNA Library Preparation: Express Genomics
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Cloning distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: NDAM599 row: k column: 12
 High quality sequence stop: 657.
 FEATURES
 source
 1. 863
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30522779"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 203"
 /note="Organ: placenta; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from three placentas from female C57/BL6 mouse at 16 days pregnancy. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer:
 5'-pGAGTAGTCTAGATCGAGCGGCCCTT)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size selection >1kb resulted in an average insert size of 1.3 kb. This primary, microquantity library is normalized to Cot5 (non-normalized primary library is NIH MGC 222) and was constructed by Express Genomics (Frederick, MD)."
 ORIGIN
 Query Match 87.9%; Score 419.4; DB 14; Length 863;
 Best Local Similarity 92.5%; Pred. No. 3.3e-105;
 Matches 441; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 Qy 1 ATGCTGGCCATGAAGCTGTTCACTTGCTTCTTGAGTCCCTAGCTGGTGGCTGGCTGCAC 60
 Db 226 ATGCTGGTCATGAAGCTGTTCACTTGCTTCTTACAGTCTAGCTGGTGGCTGGCTGCAT 285
 Qy 61 TCCAGAGGGGCCCTGCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTTCAAT 120
 Db 286 TCCAGAGGGGCCCTGCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTGGCTTTCAAC 345
 Qy 121 GAAGTGTGGGGCCGAGCTACTCGCGCCCAATGAGAGAGCTGGTGTACATTGCAGATGAA 180

Db 346 GAAGTGTGGGTCGCGAGCTACTCTGCGCCCATGAGAGAGCTGGTGTACATCTTTGGATGA 405

QY 181 CACCCTAAATGAAGTGTCTCATATATTTCAGTCCGTCTCATGTCTCTTCTGAGTGCCTGTGAGT 240

Db 406 TACCCTCATGAGTGTCTCATATATTTCAGTCCGTCTCTTCTGAGTGCCTGTGAGT 465

QY 241 GGCTGTGTGTGACGAGGCTCTGCACTGTGTGGCGCTAAAGACAGCCACATCCTATG 300

Db 466 GGCTGTGTGTGATGAAGGCTCTGCACTGTGTGGCGCTAAAGACAGCCACATCCTATG 525

QY 301 CAGATCTTAAAGATTCCCGCATTCGGATCCCATCTCTACCTGAGATGACATCTCT 360

Db 526 CAGATCTTGAAGATTCCCGCATTCGGATCCCATCTCTATGTTGAGATGACATCTCT 585

QY 361 CAGGATGTACTCTGCGAATCAGCGCTTATTCTGGACAGCAAAAGGCAGAAAGAGGAAA 420

Db 586 CAGGATGTCTCTGTGATGACACCTATTCTGGACAGCAAAAGGCAGAAAGAGGAAA 645

QY 421 ACCAAGGGGAAGAGGAGCAAAACCCACAGCTGAGGAAACCCACCTGTGA 477

Db 646 ACCAAGGGGAAGAGGAGGAGTAAACTCACAGACTGAGGAAACCCACCTGTGA 702

RESULT 5

AK042891

LOCUS

DEFINITION

AK042891 1583 bp mRNA linear HTC 19-SEP-2003

Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730035M09 product:placental growth factor, full insert sequence.

ACCESSION

AK042891

VERSION

AK042891.1 GI:26335388

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

2 9279253
10349636

REFERENCE

3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

4 20493374
11042159

REFERENCE

5 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

6 20530913
11076861

REFERENCE

7 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

8 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL REFERENCE AUTHORS

Nature 420, 563-573 (2002)

6 (bases 1 to 1583)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, Y., Kojima, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source

Location/Qualifiers

1. .1583

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM DB:A730035M09"

/db_xref="MGI:2407996"

/db_xref="taxon:10090"

/clone="A730035M09"

/tissue_type="cerebellum"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="7 days neonate"

335. .811

CDS

/note="unnamed protein product; placental growth factor (MGD|MGI:105095, GB|NM_008827, evidence: BLASTN, 100%, match=1564)

putative"

/codon_start=1

/protein_id="BAC31395.1"

/db_xref="GI:26335389"

/translation="MLVMKLTFCFLQVLAVHSQGLSAGNNSVEVVPNEVWG RYCRPMKLVILDEYDPVSHIFSPSCVLLSRGCGCGDLGHCVPKTKANITMQI LKIPNRPDPHFVEMTFSDVLCCECPILETTKAERKTKGKRKRSNSTEHPH"

1560. .1565

/note="putative"

polyA_signal

polyA_site

1583

ORIGIN

Query Match 87.9%; Score 419.4; DB 11; Length 1583;

Best Local Similarity 92.5%; Pred. No. 4.1e-105;

Matches 441; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGCTGGCCATGAAGCTGTCTTCTTCTGAGTCTCTAGCTGGTGTGGTGTGGTGCAC 60

Db 335 ATGCTGGTCTGAAGCTGTCTTCTTCTGAGTCTCTAGCTGGTGTGGTGTGGTGCAT 394

QY 61 TCCAGAGGGGCGCTGTCTCTGGGAACAACACTCAACAGAAATGGAAGTGTGCTTTCAAT 120

Db 395 TCCAGAGGGGCGCTGTCTCTGGGAACAACACTCAACAGAAATGGAAGTGTGCTTTCAAC 454

QY 121 GAAGTGTGGGCGCGAGTACTGCGGCCCAATGGAGAGCTGGTGTACATGTCAGATGAA 180

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 1579)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, F., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

TITLE
JOURNAL

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES
source
1..1579
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="FANTOM DB:E430032N09"
/db_xref="MGI:2427840"
/db_xref="taxon:10090"
/clone="E430032N09"
/cell_type="thymic cells"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="2 days neonate"
335..810
/note="placental growth factor (MGF|MGF:105095,
GB|NM_008827, evidence: BLASTN, 100%, match=1564)
putative"
polyA_signal
1559..1564
/note="putative"
polyA_site
1579
/note="putative"

ORIGIN
Query Match 85.4%; Score 407.4; DB 11; Length 1579;

Best Local Similarity 92.2%; Pred. No. 8.8e-102;
Matches 440; Conservative 0; Mismatches 36; Indels 1; Gaps 1;
1 ATGCTGGCCATGAGAGCTGTTCACTTCTTTCAGAGTCTAGCTGGTGGCTGGTGCAC 60
335 ATGCTGGTCAATGAAGCTGTTCACTTCTTTCAGAGTCTAGCTGGTGGCTGGTGCAT 393
61 TCCACAGGGGGCCCTGCTCTGCTGGGAACAACCTCAACAGAAATGAAGTGGTGCCTTTCAAT 120
394 TCCACAGGGGGCCCTGCTCTGCTGGGAACAACCTCAACAGAAATGAAGTGGTGGCTTTCAAC 453
121 GAAGTGTGGGGCCGAGCTGCTGCTGGCCCAATGGAGAGCTGTGTACATTTGAGATGAA 180
454 GAAGTGTGGGGTCCGAGCTGCTGCTGGCCCAATGGAGAGCTGTGTACATTTGAGATGAA 513
181 CACCCTTAAGTGAAGTGTCTCATATATTACAGTCCGTGCTGTGCTTCTGAGTCCGTGTAGT 240
514 TACCCTGATGAGTGTCTCATATATTACAGTCCGTGCTGTGCTTCTGAGTCCGTGTAGT 573
241 GGCTGTGTGGTACGAGGGTCTTGCACTGTGTGGCCCTAAAGACAGCCCAACATCACTATG 300
574 GGCTGTGTGGTGTGATGAAGTCTGCACTGTGTGCCGATTAAGACAGCCCAACATCACTATG 633
301 CAGATCTTAAGATTCCCCCAATCGGATGCCATTCCTACGTGAGATGACATTTCTCT 360
634 CAGATCTTAAGATTCCCCCAATCGGATGCCATTTCTATGTGGAGATGACATTTCTCT 693
361 CAGGATGTACTTGGGAATCGAGGCTTCTTGGAGACGACAAAGCAGAAAGGAGGAAA 420
694 CAGGATGTCTCTGTGAATGCGAGACCTATTCTGGAGACGACAAAGCAGAAAGGAGGAAA 753
421 ACCAAGGGGAAGAGGAAGCAAAAGCAAAACCCACACACTGAGGAACCCCACTGTGCA 477
754 ACCAAGGGGAAGAGGAGAGGAGTAGAACTCACAGACTGAGGAACCCCACTGTGCA 810

RESULT 8
CB204450 932 bp mRNA linear EST 05-FEB-2003
AGENCOURT 11276143 NIH_MGC 135 Mus musculus cDNA clone
IMAGE:30138619 5', mRNA sequence.
CB204450
VERSION CB204450.1 GI:28241906
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0041 row: 1 column: 20
High quality sequence start: 15
High quality sequence stop: 671.
Location/Qualifiers
1..932
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30138619"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_135"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRV; Site_2: NotI;

FEATURES
source
1..932
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30138619"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_135"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRV; Site_2: NotI;

Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size 1.6k bp. Normalization (Cot value): 7.5 kb. Priming sequence: 5'GACTAGTCTAGATCGGCGGCC(T)3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."

ORIGIN

Query Match 84.9%; Score 405.2; DB 14; Length 932;
Best Local Similarity 91.8%; Pred. No. 2.9e-101;
Matches 439; Conservative 0; Mismatches 38; Indels 1; Gaps 1;
QY 1 ATGCTGCCATGAAGCTGTTCACTTCTTCTGAGTCTAGTGGTGGTGGTGCAC 60
Db 350 ATGCTGCCATGAAGCTGTTCACTTCTTCTGAGTCTAGTGGTGGTGGTGCAT 409
QY 61 TCCAGGGGGCCCTGCTGCTGGGACAACTCAACAGAAATGGAAGTGGTGGTTCAT 120
Db 410 TCCAGGGGGCCCTGCTGCTGGGACAACTCAACAGAAATGGAAGTGGTGGTTCAT 469
QY 121 GAAGTGTGGGGCCGACGTAATGCGGCCAATGGAAGTGGTGGTACATTCAGATGAA 180
Db 470 GAAGTGTGGGGCCGACGTAATGCGGCCAATGGAAGTGGTGGTACATTCAGATGAA 529
QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCATGTCCTTCTGAGTGGTGTAGT 240
Db 530 TACCTGATGAGGTGTCTCATATATTCAGTCCGTCATGTCCTTCTGAGTGGTGTAGT 589
QY 241 GGCTGCTGTGAGAGGCTCTGACATGTCAGTGGCGCTTAAAGACAGCAACATCACTATG 300
Db 590 GGCTGCTGTGAGAGGCTCTGACATGTCAGTGGCGCTTAAAGACAGCAACATCACTATG 649
QY 301 CAGATCTTAAGATATCCCGCCCAATCGGATCCATTCCTACGTTGGAGATGACATTCCT 360
Db 650 CAGATCTTAAGATATCCCGCCCAATCGGATCCATTCCTACGTTGGAGATGACATTCCT 709
QY 361 CAGATGTACTCTCGAATGAGGCTTATTCGAGAGCAAAAGGCGAAGAGGAGAA 420
Db 710 CAGATGTACTCTCGAATGAGGCTTATTCGAGAGCAAAAGGCGAAGAGGAGAA 769
QY 421 ACCAA-GGGGAAGAGGAGCAAAAGCAAAACCCACAGACTGAGGACCCACCTGTGA 477
Db 770 ACCAA-GGGGAAGAGGAGCAAAAGCAAAACCCACAGACTGAGGACCCACCTGTGA 827

RESULT 9
BQ936933
LOCUS BQ936933 933 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_10017764 NCI_CGAP_Mam2 Mus musculus cDNA clone
IMAGE:6486814 5', mRNA sequence.
ACCESSION BQ936933
VERSION BQ936933.1 GI:22352316
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 933)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue procurement: Gilbert Smith, Ph.D.
cDNA Library preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM14030 row: m column: 23
High quality sequence stop: 691.

FEATURES
source

Location/Qualifiers
1. .933
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:6486814"
/tissue type="tumor, biopsy sample"
/dev stage="5 months"
/lab_host="DH10B"
/clone_11b="NCI_CGAP_Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 84.9%; Score 405.2; DB 13; Length 933;
Best Local Similarity 91.8%; Pred. No. 2.9e-101;
Matches 439; Conservative 0; Mismatches 38; Indels 1; Gaps 1;
QY 1 ATGCTGCCATGAAGCTGTTCACTTCTTCTGAGTCTAGTGGTGGTGGTGCAC 60
Db 317 ATGCTGCCATGAAGCTGTTCACTTCTTCTGAGTCTAGTGGTGGTGGTGCAT 376
QY 61 TCCAGGGGGCCCTGCTGCTGGGACAACTCAACAGAAATGGAAGTGGTGGTTCAT 120
Db 377 TCCAGGGGGCCCTGCTGCTGGGACAACTCAACAGAAATGGAAGTGGTGGTTCAT 436
QY 121 GAAGTGTGGGGCCGACGTAATGCGGCCAATGGAAGTGGTGGTACATTCAGATGAA 180
Db 437 GAAGTGTGGGGCCGACGTAATGCGGCCAATGGAAGTGGTGGTACATTCAGATGAA 496
QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCATGTCCTTCTGAGTGGTGTAGT 240
Db 497 TACCTGATGAGGTGTCTCATATATTCAGTCCGTCATGTCCTTCTGAGTGGTGTAGT 556
QY 241 GGCTGCTGTGAGAGGCTCTGACATGTCAGTGGCGCTTAAAGACAGCAACATCACTATG 300
Db 557 GGCTGCTGTGAGAGGCTCTGACATGTCAGTGGCGCTTAAAGACAGCAACATCACTATG 616
QY 301 CAGATCTTAAGATATCCCGCCCAATCGGATCCATTCCTACGTTGGAGATGACATTCCT 360
Db 617 CAGATCTTAAGATATCCCGCCCAATCGGATCCATTCCTACGTTGGAGATGACATTCCT 676
QY 361 CAGATGTACTCTCGAATGAGGCTTATTCGAGAGCAAAAGGCGAAGAGGAGAA 420
Db 677 CAGATGTACTCTCGAATGAGGCTTATTCGAGAGCAAAAGGCGAAGAGGAGAA 736
QY 421 ACCAA-GGGGAAGAGGAGCAAAAGCAAAACCCACAGACTGAGGACCCACCTGTGA 477
Db 737 ACCAA-GGGGAAGAGGAGCAAAAGCAAAACCCACAGACTGAGGACCCACCTGTGA 794

RESULT 10
BQ936933
LOCUS BQ936933 744 bp mRNA linear EST 12-SEP-2001
DEFINITION 603288511F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5322603 5', mRNA sequence.
ACCESSION BQ936933
VERSION BQ936933.1 GI:15578005
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 744)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.


```

Db      345 CAGATCTTGAAGATCCCCCAATCGGATCCACATTTCTATGTGGAGATGACATTTTCT 404
QY      361 CAGATGTAATCTCGAATCGAGGCTATTCTCGAGACGACAAAGGAGAA 411
Db      405 CAGGATGTCTGTGAATGACACCTTATTCTGGAGACGACAAAGGAGAA 455

RESULT 12
LOCUS   BI685632
DEFINITION
603309146F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345050 5',
mRNA sequence.
ACCESSION
BI685632
VERSION  BI685632.1 GI:15648260
KEYWORDS
EST.
SOURCE  Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 759)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-i@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1876 row: 1 column: 11
High quality sequence stop: 756.
FEATURES
source
1..759
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5345050"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
Query Match 75.8%; Score 361.8; DB 12; Length 759;
Best Local Similarity 92.2%; Pred. NO. 2.9e-89;
Matches 392; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY      1 ATGCTGGCCATGAAGCTGTTCACTTGCTTCTTGGAGTCCCTAGCTGGGTGGCTGTGCAC 60
Db      335 ATGCTGGTCATGAAGCTGTTCACTTGCTTCTTACAGGTCCTAGCTGGGTGGCTGTGCAT 394
QY      61 TCCAGAGGGGGCCCTGCTGCTGGGAACAACTCAACAGAAATGGAAGTGGTGGCTTTCAAT 120
Db      395 TCCAGAGGGGGCCCTGCTGCTGGGAACAACTCAACAGAAATGGAAGTGGTGGCTTTCAAC 454
QY      121 GAAAGTGTGGGGCCGAGCTACTGCGGCCCAATGGAAGAGCTGGTGTACATTGCGAGAA 180
Db      455 GAAAGTGTGGGGTCGAGCTACTGTCGGCCCAATGGAAGAGCTGGTGTACATTGCGAGAA 514
QY      181 CACCCATATGAAGTGTCTATATATTCAGTCGGTTCATGTCCTCTCTGAGTCGCTGTAGT 240
Db      515 TACCCCTGATGAGGTGTCTACATATTCAGTCGGTTCCTCTCTGAGTCGCTGTAGT 574
QY      241 GGCTGCTGTGGGTGACGAGGGTCTGCATCTGTGTGGGGCTAAAGACAGCAACATCACTATG 300

```

```

Db      575 GGCTGCTGTGGTGAAGGTCCTGCACCTGTGTCCGATAAAGACAGCAACATCACTATG 634
QY      301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTTCTACCTCGT-GGAGATGACATTTCTC 359
Db      635 CAGATCTTGAAGATTCCTCCCAATCGGATCCACATTTCTATGTGGAGATGACATTTTC 694
QY      360 TCAGGATGTAATCTCGAATGCGAGGCTATTCTGGAGACGACAAAGGAGAGGAA 419
Db      695 TCAGGATGTAATCTCGAATGCGAGGCTATTCTGGAGACGACAAAGGAGAGGAA 754
QY      420 AACCA 424
Db      755 AACCA 759

RESULT 13
LOCUS   BI790853
DEFINITION
id09h10.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
musculus cDNA clone IMAGE:5662723 5' similar to SW:PLGF_MOUSE
P49764 PLACENTA GROWTH FACTOR PRECURSOR ;, mRNA sequence.
ACCESSION
BI790853
VERSION  BI790853.1 GI:15818578
KEYWORDS
EST.
SOURCE  Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 489)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE   Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:1949049 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 429.
FEATURES
source
1..489
/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5662723"
/sex="Both for embryonic & newborn, male for adult and
adult islet"
/dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
adult, mixed"
/lab_host="DH10B"
/clone_lib="Melton Normalized Mixed Mouse Pancreas 1
N1-MMS1"
/notes="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five
libraries representing B10.5/12.5 pancreatic bud, B16.5
pancreas, newborn pancreas, adult pancreas, and adult
islets of Langerhans were separately constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA

```

COMMENT

BE1108026 308 bp mRNA linear EST 26-JUN-2001
 6029024039F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5031842 5',
 mRNA sequence.
 BE1108026
 BE1108026.1 GI:14558919
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 908)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM11089 row: b column: 03
 High quality sequence stop: 788.
 Location/Qualifiers

FEATURES

1..908
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129, C57BL/6J, FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5031842"
 /tissue_type="tumor, gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Mam3"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: Sali;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

ORIGIN

Query Match 75.2%; Score 358.8; DB 12; Length 908;
 Best Local Similarity 90.0%; Pred. No. 2.1e-88;
 Matches 430; Conservative 0; Mismatches 42; Indels 6; Gaps 4;
 Qy 1 ATGCTGCCCATGAGCTGTTACACTGCTCTTCTGCGAGTCCCTAGCTGGTGGCTGTGCAC 60
 Db 314 ATGCTGGTCATGAAGCTGTTACACTGCTCTTCTGCGAGTCCCTAGCTGGTGGCTGTGCAT 373
 Qy 61 TCCAGGGGGCCCTGTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTCAAT 120
 Db 374 TCCAGGGGGCCCTGTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTCAAC 433
 Qy 121 GAAGTGTGGGCGCAGCTACTGCGGCCCAATGAGAAAGCTGGTGTACATTGCGAGTAA 180
 Db 434 GAAGTGTGGGCTCGCAGCTACTGTCGGCCCATGGAGAAGCTGGTGTACATCTTGGATGA 493
 Qy 181 CACCTATATGAGTGTCTCATATATTACATCGTCCATCTGCTCTGAGTCCCTGTAGT 240
 Db 494 TACCTGATGAGGTGTCTCATATATTACATATTCAGTCCGTCCTGCTCTGAGTCCCTGTAGT 553
 Qy 241 GGCTGCTGTGTGACGAGGCTCTGCACTGTGTGGCGCTAAAGACAGCCCAACATCACTATG 300
 Db 554 GGCTGCTGTGTGATGAAGGTCTGCACTGTGTGGCGCTAAAGACAGCCCAACATCACTATG 613
 Qy 301 CAGATCTTTAAG-ATTCCCCCAATCGGGATCCCAATTCTACGTGGAGATGACATTCTC 359
 Db 614 CAGATCTTTGAAGATTCCCCCAATCGGGATCCCAATTCTATGTGGAGATGACATTTTC 673
 Qy 360 TCAGGATG-TACTCTCGAATCAGGCCCTATTCTGGAGCAGCAAGG--CAGAAGGAG 416
 Db 674 TCAGGATGTGCTCTGTGAATCCGACCTATTCTGGAGCAGCAAGGCGCCGAAGGGGAG 733
 Qy 417 GAAACCAAGGGGAAGA--GGAAGCAAAAGCAAAACCCACAGACTGAGGAACCCACC 472
 Db 734 GAAACCAAGGGGAAGAGAGAGCGGAGTAGAAGTACAGACTGAGGAACCCACC 791

Search completed: September 16, 2004, 21:26:53
 Job time : 2002 secs

Blank Sheet (05570)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 19:52:03 ; Search time 64 Seconds
(without alignments)
4136.118 Million cell updates/sec

Title: US-10-071-370A-3

Perfect score: 477

Sequence: 1 atgtggccatgaagctgtt.....ctgaggaaacccacctgtga 477

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
 - 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 - 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
 - 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
 - 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	100.0	477	3	US-08-586-039B-38
2	477	100.0	477	4	US-09-699-769-38
3	414	86.8	417	3	US-08-586-039B-36
4	414	86.8	417	4	US-09-699-769-36
5	230.2	48.3	513	3	US-08-586-039B-44
6	230.2	48.3	513	4	US-09-699-769-44
7	229.8	48.2	465	3	US-08-586-039B-40
8	229.8	48.2	465	4	US-09-699-769-40
9	213.6	44.8	1645	2	US-08-039-297B-1
10	213.2	44.7	450	3	US-08-586-039B-46
11	213.2	44.7	450	4	US-09-699-769-46
12	108.8	22.8	677	3	US-08-718-904-3
13	108.8	22.8	677	4	US-09-449-249-3
14	108.8	22.8	677	5	PCT-US95-10973A-27
15	108.8	22.8	728	3	US-08-718-904-4
16	108.8	22.8	728	4	US-09-449-249-4
17	108.8	22.8	728	5	PCT-US95-10973A-28
18	107.2	22.5	495	4	US-09-037-983C-14
19	107.2	22.5	516	3	US-08-784-551C-1
20	107.2	22.5	516	4	US-09-392-932-7
21	107.2	22.5	516	4	US-09-574-708A-3
22	107.2	22.5	516	4	US-09-037-983C-1
23	107.2	22.5	516	4	US-09-428-909A-1
24	107.2	22.5	516	4	US-09-392-931-3
25	107.2	22.5	545	4	US-09-244-583-1
26	107.2	22.5	642	4	US-09-392-932-9
27	107.2	22.5	642	4	US-09-574-708A-7

28	107.2	22.5	642	4	US-09-392-931-7	Sequence 7, Appli
29	107.2	22.5	648	3	US-08-586-039B-48	Sequence 48, Appl
30	107.2	22.5	648	4	US-09-699-769-48	Sequence 48, Appl
31	107.2	22.5	665	4	US-09-244-583-29	Sequence 29, Appl
32	107.2	22.5	699	4	US-09-392-932-10	Sequence 10, Appl
33	107.2	22.5	699	4	US-09-574-708A-9	Sequence 9, Appli
34	107.2	22.5	699	4	US-09-392-931-9	Sequence 9, Appli
35	107.2	22.5	1195	6	5240848-6	Patent No. 5240848
36	106	22.2	649	3	US-08-586-039B-34	Sequence 34, Appl
37	106	22.2	649	4	US-09-699-769-34	Sequence 34, Appl
38	105.6	22.1	495	4	US-09-244-583-25	Sequence 25, Appl
39	105.6	22.1	627	4	US-09-244-583-27	Sequence 27, Appl
40	105.6	22.1	649	4	US-09-519-476-1	Sequence 1, Appli
41	105.2	22.1	444	4	US-09-392-932-6	Sequence 6, Appli
42	105.2	22.1	444	4	US-09-574-708A-1	Sequence 1, Appli
43	105.2	22.1	444	4	US-09-392-931-1	Sequence 1, Appli
44	105.2	22.1	456	5	PCT-US95-10973A-88	Sequence 88, Appl
45	105.2	22.1	467	5	PCT-US95-10973A-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-08-586-039B-38
; Sequence 38, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas, Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,039B
FILING DATE: 16-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/124,259
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-586-039B-38

Query Match 100.0%; Score 477; DB 3; Length 477;
Best Local Similarity 100.0%; Fred. No. 9.8e-149; Mismatches 0; Indels 0; Gaps 0;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/124,259
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-586-039B-36

Query Match 86.8%; Score 414; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 8.1e-128;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCCCATGAAGCTGTTCACTTGTCTTGTGAGGTCCTAGCTGGGTGGCTGTGCAC 60
Db 1 ATGCTGCCCATGAAGCTGTTCACTTGTCTTGTGAGGTCCTAGCTGGGTGGCTGTGCAC 60
QY 61 TCCAGAGGGGCGCTGTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTCAAT 120
Db 61 TCCAGAGGGGCGCTGTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTCAAT 120
QY 121 GAAGTGTGGGCGCGAGCTACTGCGGCAATGGAAGCTGGTGTACATTCGAGATGAA 180
Db 121 GAAGTGTGGGCGCGAGCTACTGCGGCAATGGAAGCTGGTGTACATTCGAGATGAA 180
QY 181 CACCTTAATGAAGTGTCTCATATATTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 CACCTTAATGAAGTGTCTCATATATTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GCCTGCTGTGTGAGAGGGTCTGCACCTGTGTGGCGCTTAAAGACAGCCAAATCACTATG 300
Db 241 GCCTGCTGTGTGAGAGGGTCTGCACCTGTGTGGCGCTTAAAGACAGCCAAATCACTATG 300
QY 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTAGCTGGAGATGACATTCCTCT 360
Db 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTAGCTGGAGATGACATTCCTCT 360
QY 361 CAGGATGTACTCTGCGAATGAGGCTATTCTGGAGACGACAAAGGCGAAGG 414
Db 361 CAGGATGTACTCTGCGAATGAGGCTATTCTGGAGACGACAAAGGCGAAGG 414

RESULT 4

US-09-699-769-36
Sequence 36, Application US/09699769
Patent No. 6569434
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
Thomas Jr., Kenneth A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/699,769
FILING DATE: 30-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/586,039
FILING DATE: 16-JAN-1996
APPLICATION NUMBER: 08/124,259
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-3905
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-699-769-36

Query Match 86.8%; Score 414; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 8.1e-128;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCCCATGAAGCTGTTCACTTGTCTTGTGAGGTCCTAGCTGGGTGGCTGTGCAC 60
Db 1 ATGCTGCCCATGAAGCTGTTCACTTGTCTTGTGAGGTCCTAGCTGGGTGGCTGTGCAC 60
QY 61 TCCAGAGGGGCGCTGTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTCAAT 120
Db 61 TCCAGAGGGGCGCTGTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTCAAT 120
QY 121 GAAGTGTGGGCGCGAGCTACTGCGGCAATGGAAGCTGGTGTACATTCGAGATGAA 180
Db 121 GAAGTGTGGGCGCGAGCTACTGCGGCAATGGAAGCTGGTGTACATTCGAGATGAA 180
QY 181 CACCTTAATGAAGTGTCTCATATATTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 CACCTTAATGAAGTGTCTCATATATTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GCCTGCTGTGTGAGAGGGTCTGCACCTGTGTGGCGCTTAAAGACAGCCAAATCACTATG 300
Db 241 GCCTGCTGTGTGAGAGGGTCTGCACCTGTGTGGCGCTTAAAGACAGCCAAATCACTATG 300
QY 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTAGCTGGAGATGACATTCCTCT 360
Db 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTAGCTGGAGATGACATTCCTCT 360
QY 361 CAGGATGTACTCTGCGAATGAGGCTATTCTGGAGACGACAAAGGCGAAGG 414
Db 361 CAGGATGTACTCTGCGAATGAGGCTATTCTGGAGACGACAAAGGCGAAGG 414

RESULT 5

US-08-586-039B-44
Sequence 44, Application US/08586039B
Patent No. 6140073
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
APPLICANT: Thomas Jr., Kenneth A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C

;; TITLE OF INVENTION: SUBUNIT
;; NUMBER OF SEQUENCES: 49
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Merck & Co., Inc.
;; STREET: 126 E. Lincoln Avenue
;; CITY: Rahway
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07065-0900
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Microsoft Word 6
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/586,039B
;; FILING DATE: 16-JAN-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/124,259
;; FILING DATE: 20-SEP-1993
;; APPLICATION NUMBER: 07/676,436
;; FILING DATE: 28-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hand, J. Mark
;; REGISTRATION NUMBER: 36,545
;; REFERENCE/DOCKET NUMBER: 18361DA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (908) 594-3905
;; TELEFAX: (908) 594-4720
;; INFORMATION FOR SEQ ID NO: 44:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 513 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-586-039B-44

Query Match 48.3%; Score 230.2; DB 3; Length 513;
Best Local Similarity 71.6%; Pred. No. 1.2e-66;
Matches 336; Conservative 0; Mismatches 118; Indels 15; Gaps 2;

QY 1 ATGCTGGCCATGAAGCTGTTCACTGCTTTTCGAGGTCCTAGCTGGTTGGCTGTGCAC 60
Db 1 ATGCGGTCTATGAGGCTGTTCCCTGCTTCTCAGCTCTCTGCGGGCTGGCGCTGCCT 60

QY 61 TCC-----CAGGGGGCCCTGCTGCTGGGAAACAACCTCAACAGAAATGGAAGTG 108
Db 61 GCTGTGCCCCCAGAGTGGGCTTGTCTGTGGGAAACGGCTCGTCAGAGGTGGAAGTG 120

QY 109 GTGCCCTTTCAATGAAGTGTGGGCGCAGCTACTGCGGCGCAATGGAGAGCTGTGTGAC 168
Db 121 GTACCCCTTCAGGAAGTGTGGGCGCAGCTACTGCGGCGCGCTGGAGAGGCTGTGGAC 180

QY 169 ATTGCAGATGAACCCCTAATGAAGTGTCTATATATTAGTCCCGTCATGTGTCTCTTG 228
Db 181 GTGCTGTCGAGTACCGGCGCTGCTGCTGAGTGTGGGCGCTGCTGAGAGGCTGTGGGAC 240

QY 229 AGTCGCTGTAGTGGCTGTGTGTGACGAGGGTCTGCACTGTGTGGCGCTAAAGACAGCC 288
Db 241 CTGCGCTGTACCGGCTGTGCGGCGATGAGATCTGCACTGTGTGGCGCTGAGAGCGGCC 300

QY 289 ACATCACTATGAGATCTTAAGATTCGCCCAATCGGATCCACATTCCTACGTGGAG 348
Db 301 AATGTCAACATGAGCTCTCAAGAT---CCGTTCTGGGGAACCGGCCCTCTCACTGTGGAG 357

QY 349 ATGACATTTCTCAGAGTGTACTCTCGAATGACGCGCTATTCTTGAGACGACAAAGCA 408
Db 358 CTGACGTTCTCTCAGACAGTTCGCTCGAATGCGGCGCTCTGCGGAGAGATGAAGCGC 417

QY 409 GAAAGGAGAAACCAAGGGGAGAGAGAAAGCAAGCAAAACCCACAGA 457
|||||

Db 418 GAAAGGAGAGAGACCCCAAGGCGAGGGGGAAGAGAGAGAGAGAGAGCAGA 466

RESULT 6
US-09-699-769-44
; Sequence 44, Application US/09699769
; Patent No. 6569434
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
; C SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/699,769
; FILING DATE: 30-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/586,039
; FILING DATE: 16-JAN-1996
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732) 594-3905
; TELEFAX: (732) 594-4720
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-699-769-44

Query Match 48.3%; Score 230.2; DB 4; Length 513;
Best Local Similarity 71.6%; Pred. No. 1.2e-66;
Matches 336; Conservative 0; Mismatches 118; Indels 15; Gaps 2;

QY 1 ATGCTGGCCATGAAGCTGTTCACTGCTTTTCGAGGTCCTAGCTGGTTGGCTGTGCAC 60
Db 1 ATGCGGTCTATGAGGCTGTTCCCTGCTTCTCAGCTCTCTGCGGGCTGGCGCTGCCT 60

QY 61 TCC-----CAGGGGGCCCTGCTGCTGGGAAACAACCTCAACAGAAATGGAAGTG 108
Db 61 GCTGTGCCCCCAGAGTGGGCGCTTGTCTGTGGGAAACGGCTCGTCAGAGGTGGAAGTG 120

QY 109 GTGCCCTTTCAATGAAGTGTGGGCGCAGCTACTGCGGCGCAATGGAGAGCTGTGTGAC 168
Db 121 GTACCCCTTCAGGAAGTGTGGGCGCAGCTACTGCGGCGCGCTGGAGAGGCTGTGGGAC 180

QY 169 ATTGCAGATGAACCCCTAATGAAGTGTCTATATATTAGTCCCGTCATGTGTCTCTTG 228
Db 181 GTGCTGTCGAGTACCGGCGCTGCTGCTGAGTGTGGGCGCTGCTGAGAGGCTGTGGGAC 240

QY 229 AGTCGGCTGTAGTGGCTGCTGTGGTACGAGGGTCTGCACTGTGTGGCGCTAAAGACAGCC 288
DB 241 CTCGGCTGACCGCTGTCTGCGCGATGAGAACTGCACTGTGTGCGGTGGAGACGGCC 300
QY 289 AACATCACTATGAGATCTTAAAGATCCCGCAATCGGATCCACATTCCTACGTGGAG 348
DB 301 AATGTCACCATGAGCTCTCTAAAGAT---CCGTTCTGGGACCGGCCCTCTACGTGGAG 357
QY 349 ATGACATCTCTCAGGATGTACTCTGGAATGAGGCTTATCTGGAGAGCAAAAGGCA 408
DB 358 CTGACGTTCTCTCAGCACGTTGCTGGAATGCGGCTCTGCGGAGAGATGAAGCCG 417
QY 409 GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 457
DB 418 GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 466

RESULT 7
US-08-586-039B-40
; Sequence 40, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-586-039B-40
Query Match 48.2%; Score 229.8; DB 3; Length 465;
Best Local Similarity 72.3%; Pred. No. 1.5e-66;
Matches 332; Conservative 0; Mismatches 112; Indels 15; Gaps 2;

QY 1 ATGCTGGCCATGAGCTGTCTACTTCTTGGAGTCTAGTGGTGGTGGTGGTGGTGGTGGTGG 60
DB 1 ATGCGGTGATGAGGCTGTCT 60
QY 61 TCC-----CAGGGGGCCCTGTCTGTCTGGGAAACAACACTCAACAGAAATGGAAGTG 108

DB 61 GTGTGCCCCCAGCAGTGGGCTTGTCTGTGGGAAACGGCTCTGTCAGAGTGGAAAGTG 120
QY 109 GTCCCTTTCAATGAAGTGTGGGCGCCAGCTACTGCGCGCAATGGAAGCTGGTGTAC 168
DB 121 GTACCTTTCCAGAAAGTGTGGGCGCCAGCTACTGCGGCGCTGGAGAGCTGGTGGAC 180
QY 169 ATTGCAGATGAACACCCCTAATGAAGTGTCTCATATATTCAGTCCGTTCATGTCTCTG 228
DB 181 GTCGTGTCCGAGTACCCAGCGAGGTGGAGCATGTTACGCCCATCTGTCTCTCCCTG 240
QY 229 AGTCGGCTGTAGTGGCTGCTGTGTCGACGAGGTCTGCACGTGTGGCGCTAAAGACAGCC 288
DB 241 CTGCGTGTGACCGGCTGCTGCGCGATGAGAAATCTGCACGTGTGCGCGTGGAGACGGCC 300
QY 289 AACATCACTATGAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTACGTGGAG 348
DB 301 AATGTCACCATGAGCTCTCTAAAGAT---CCGTTCTGGGACCGGCCCTCTACGTGGAG 357
QY 349 ATGACATCTCTCAGGATGTACTCTGGAATGAGGCTTATCTGGAGAGCAAAAGGCA 408
DB 358 CTGACGTTCTCTCAGCACGTTGCTGGAATGCGGCTCTGCGGAGAGATGAAGCCG 417
QY 409 GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 447
DB 418 GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 456

RESULT 8
US-09-699-769-40
; Sequence 40, Application US/09699769
; Patent No. 6569434
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/699,769
; FILING DATE: 30-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/586,039
; FILING DATE: 16-JAN-1996
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732) 594-3905
; TELEFAX: (732) 594-4720
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

RESULT 10
US-08-586-039B-46
; Sequence 46: Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA

```

RESULT 10
US-08-586-039E-46
; Sequence 46. Application US/08586039B
; Patent No. 6140073
;
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDO
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA

```

```

;
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-586-039B-46

```

```

Query Match 44.7%; Score 213.2; DB 3; Length 450;
Best Local Similarity 72.4%; Pred. No. 5e-61;
Matches 310; Conservative 0; Mismatches 103; Indels 15; Gaps 2;

QY 1 ATGCTGGCCATGAAGCTGTTACCTTCTTCTGAGGCTCCTAGCTGGTGGCTGTGCAC 60
Db 1 ATGCGGGTCATGAGGCTGTTCCCTTGTCTTCTGAGGCTCCTGGCGGGCTGGCGCTGCT 60
QY 61 TCC-----CAGGGGGCCCTGTCCTGCGGAACAACCTCAACAGAAATGGAAGTG 108
Db 61 GCTGTGCCCCCCCCAGAGCTGGGCGCTTGTCTGCTGGGAACGCTCTGTAGAGTGAAGTG 120
QY 109 GTGCTTTTCAATGAAGTGTGGGGCGGCGAGCTACTGCCGCCCAATGGAGAAGTGTGTAC 168
Db 121 GTACCTTCCAGGAAGTGTGGGGCGGCGAGCTACTGCCGCCCAATGGAGAAGTGTGTAC 168
QY 169 ATTGAGATGAACCCCTTAATGAAGTGTCTCATATATTTCAGTCCGTATGTCTCTTCTG 228
Db 181 GTCGTGTCGAGTACCCCGAGGAGTGAGACATGTTTCAGCCCATCTCTGTCTCTCCCTG 240
QY 229 AGTCGTGTAGTGGCTGCTGTGTCAGGAGGTCGTGCTGTCGCGGCTAAAGACAGCC 288
Db 241 CTGGCTGCACCGGCTGCTGCGGCGATGAGAACTGTGTCGCCCGGCTGAGAGAGGCC 300
QY 289 AACATCACTATGAGATCTTAAAGATTCGCCCAATCGGGATTCACATTCCTACGTGGAG 348
Db 301 AATGTACCATGACGCTCTCTAAAGAT---CCGTTCTGGGGACCGGCCCTCTCTACGTGGAG 357
QY 349 ATGACATTCTCTCAGATGTAATCTTGGAAATGAGGCTTCTTGGAGACGACAAAGGCA 408
Db 358 CTGACGTTCTCTCAGACAGCTTCCGCTGCGAATGCGCGCTCTGCGGAGAAATGAAGCC 417
QY 409 GAAAGGAG 416
Db 418 GAAAGGTG 425

```

```

RESULT 11
US-09-699-769-46
; Sequence 46, Application US/09699769
; Patent No. 6569434
; GENERAL INFORMATION:

```

```

;
; APPLICANT: Bayne, Marvin L.
; Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
; C SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/699,769
; FILING DATE: 30-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/586,039
; FILING DATE: 16-JAN-1996
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732) 594-3905
; TELEFAX: (732) 594-4720
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
; US-09-699-769-46

```

```

Query Match 44.7%; Score 213.2; DB 4; Length 450;
Best Local Similarity 72.4%; Pred. No. 5e-61;
Matches 310; Conservative 0; Mismatches 103; Indels 15; Gaps 2;

QY 1 ATGCTGGCCATGAAGCTGTTACCTTCTTCTGAGGCTCCTAGCTGGTGGCTGTGCAC 60
Db 1 ATGCGGGTCATGAGGCTGTTCCCTTGTCTTCTGAGGCTCCTGGCGGGCTGGCGCTGCT 60
QY 61 TCC-----CAGGGGGCCCTGTCCTGCGGAACAACCTCAACAGAAATGGAAGTG 108
Db 61 GCTGTGCCCCCCCCAGAGCTGGGCGCTTGTCTGCTGGGAACGCTCTGTAGAGTGAAGTG 120
QY 109 GTGCTTTTCAATGAAGTGTGGGGCGGCGAGCTACTGCCGCCCAATGGAGAAGTGTGTAC 168
Db 121 GTACCTTCCAGGAAGTGTGGGGCGGCGAGCTACTGCCGCCCAATGGAGAAGTGTGTAC 168
QY 169 ATTGAGATGAACCCCTTAATGAAGTGTCTCATATATTTCAGTCCGTATGTCTCTTCTG 228
Db 181 GTCGTGTCGAGTACCCCGAGGAGTGAGACATGTTTCAGCCCATCTCTGTCTCTCCCTG 240
QY 229 AGTCGTGTAGTGGCTGCTGTGTCAGGAGGTCGTGCTGTCGCGGCTAAAGACAGCC 288
Db 241 CTGGCTGCACCGGCTGCTGCGGCGATGAGAACTGTGTCGCCCGGCTGAGAGAGGCC 300
QY 289 AACATCACTATGAGATCTTAAAGATTCGCCCAATCGGGATTCACATTCCTACGTGGAG 348
Db 301 AATGTACCATGACGCTCTCTAAAGAT---CCGTTCTGGGGACCGGCCCTCTCTACGTGGAG 357

```

QY 349 ATGACATCTCTCAGGATGTAATCGAATGAGGCTTATCTGGAGAGCAACAAAGGCA 408
 Db 358 CTGACGTCTCTCAGCAGCTTCTGCTGCAATGCGGCTCTGCGGAGAAAGATGAAGCG 417
 QY 409 GAAAGGAG 416
 Db 418 GAAAGGTG 425

RESULT 12
 US-08-718-904-3
 ; Sequence 3, Application US/08718904
 ; Patent No. 6037329
 ; GENERAL INFORMATION:
 ; APPLICANT: Baird, J. Andrew
 ; APPLICANT: Chandler, Lois Ann
 ; APPLICANT: Sosnowski, Barbara A.
 ; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
 ; NUMBER OF SEQUENCES: 128
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/718,904
 ; FILING DATE: 24-SEP-1996
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6037329tenburg Ph.D., Carol
 ; REGISTRATION NUMBER: 39,317
 ; REFERENCE/DOCKET NUMBER: 760100.415C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 677 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 13..657
 ; OTHER INFORMATION: /product= "VEGF189-encoding DNA"
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 13..90
 ; OTHER INFORMATION: /product= "leader sequence-encoding DNA"
 ; US-08-718-904-3

Query Match 22.8%; Score 108.8; DB 3; Length 677;
 Best Local Similarity 59.8%; Pred. No. 3.2e-26;
 Matches 201; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

QY 103 GAAGTGTGCTTTCAATGAAGTGTGGGCGCAGCTACTGCGGCCAATGGAGAGCTG 162
 Db 127 GAAGTGTGAAGTTCATGATGCTATCATCGCAGCTACTGCCATCCATCGAGACCTG 186
 QY 163 GGTGACATTCGAGATGAACCCCTAATGAAGTGTCTCATATATTAGTCCGTATGTGC 222
 Db 187 GTGGACATCTTCAGAGTACCTCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTG 246
 QY 223 CTCTGAGTGCCTGTAGTGTGCTGCTGTGTGACGAGGGTCTGCACCTGTGTGGCGCTAAAG 282

Db 247 CCCCTGATGCGATGCGGGGCTGCTGCAATGACGAGGGCCCTGGAGTGTGTGCCACTGAG 306
 QY 283 ACAGCCAACTACTATGCGAGATCTTAAAGATTCCTCCCTCCCAATCGGATCCACATTCCTAC 342
 Db 307 GAGTCCAACTACCATGCGAGATTCGCGATCAACCTCACCAGGCCAGCA---CATA 363
 QY 343 GTGGAGATGACATTTCTCTCAGGATGTAATCTGGAATGCGAGGCTTATCTGGAGACGACA 402
 Db 364 GGAGAGATGAGCTTCTTACAGCACACAAATGTGATGCGAGACCAAGAAGGATAGAGCA 423
 QY 403 AAGCGAAGAGGAGGAAACCAAGGGGAAGGAAG 438
 Db 424 AGACAAGAAAAAATCAGTTTCGAGGAAGGGAAG 459

RESULT 13
 US-09-449-249-3
 ; Sequence 3, Application US/09449249
 ; Patent No. 6503886
 ; GENERAL INFORMATION:
 ; APPLICANT: Baird, J. Andrew
 ; APPLICANT: Chandler, Lois Ann
 ; APPLICANT: Sosnowski, Barbara A.
 ; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA
 ; NUMBER OF SEQUENCES: 128
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/449,249
 ; FILING DATE: 24-NOV-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/718,904
 ; FILING DATE: 24-SEP-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6503886tenburg Ph.D., Carol
 ; REGISTRATION NUMBER: 39,317
 ; REFERENCE/DOCKET NUMBER: 760100.415C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 677 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 13..657
 ; OTHER INFORMATION: /product= "VEGF189-encoding DNA"
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 13..90
 ; OTHER INFORMATION: /product= "leader sequence-encoding DNA"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ; US-09-449-249-3

Query Match 22.8%; Score 108.8; DB 4; Length 677;
 Best Local Similarity 59.8%; Pred. No. 3.2e-26;
 Matches 201; Conservative 0; Mismatches 132; Indels 3; Gaps 1;


```
; NAME/KEY: CDS
; LOCATION: 13..90
; OTHER INFORMATION: /product= leader sequence encoding DNA
US-08-718-904-4

Query Match      22.8%; Score 108.8; DB 3; Length 728;
Best Local Similarity 59.8%; Pred. No. 3.4e-26;
Matches 201; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

QY 103 GAAGTGTGCTTTCAATGAAGTGTGGGGCGGCGAGCTACTGCGGCCCAATGGAGAAGCTG 162
Db 127 GAAGTGTGAAGTTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCATCGAGACCCTG 186

QY 163 GTGTACATTGCAGATGAACACCCCTAATGAAGTGTCTCATATATTTCAGTCCGTCAATGTTC 222
Db 187 GTGGACATCTTCCAGGAGTACCCTGATGATCGAGTACATCTTCAAGCCATCCTGTGTG 246

QY 223 CTCTGTAGTCGCTGTAGTGGCTGCTGTGGTGACGAGGGTCTGCACCTGTGTGGCGCTAAAG 282
Db 247 CCCCTGATGCGATGCGGGGCTGCTGCAATGACGAGGGCTGGAGTGTGCCCACTGAG 306

QY 283 ACAGCCAACTACTATGCAGATCTTAAAGATTCCCGCCCAATCGGGATCCACATTCCTAC 342
Db 307 GAGTCCAACTACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCA---CATA 363

QY 343 GTGGAGATGACATTCTCTCAGGATGTACTCTGCGAATGCGAGGCTATTCTGGAGACGACA 402
Db 364 GGAGAGATGAGCTTCTCTACAGCACACAAATGTCAATGCAGACCAAGAGGATAGAGCA 423

QY 403 AAGGCAGAAAGGAGGAAACCAAGGGGAAGGGAAG 438
Db 424 AGACAGAAAAAATAATCAGTTCAGGAAAGGGAAG 459
```

Search completed: September 16, 2004, 21:28:03
Job time : 65 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 17:54:38 ; Search time 2305 seconds
(without alignments)
8969.470 Million cell updates/sec

Title: US-10-071-370A-3

Perfect score: 477

Sequence: 1 atgtggccatgaagctgtt.....ctgagggaacccacctgtga 477

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**

2: gb_hg:**

3: gb_in:**

4: gb_om:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pl:**

9: gb_pr:**

10: gb_ro:**

11: gb_sts:**

12: gb_sy:**

13: gb_un:**

14: gb_vi:**

15: em_ba:**

16: em_fun:**

17: em_hum:**

18: em_in:**

19: em_mu:**

20: em_om:**

21: em_or:**

22: em_ov:**

23: em_pat:**

24: em_ph:**

25: em_pl:**

26: em_ro:**

27: em_sts:**

28: em_un:**

29: em_vi:**

30: em_htg_hum:**

31: em_htg_inv:**

32: em_htg_other:**

33: em_htg_mus:**

34: em_htg_pln:**

35: em_htg_rod:**

36: em_htg_mam:**

37: em_htg_vrt:**

38: em_sy:**

39: em_htgo_hum:**

40: em_htgo_mus:**

41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	477	100.0	477	6	AR117110	AR117110 Sequence
2	477	100.0	477	6	AR338153	AR338153 Sequence
3	475.4	99.7	665	10	RAUPLGF	L40030 Rattus norv
4	419.4	87.9	1370	10	MMP1GF	X80171 Mus musculus
5	419.4	87.9	1580	10	MMP1GF	X96933 M.musculus
6	419.4	87.9	1674	10	BC016567	BC016567 Mus muscu
7	414	86.8	417	6	AR117109	AR117109 Sequence
8	414	86.8	417	6	AR338152	AR338152 Sequence
9	230.2	48.3	513	6	AR117114	AR117114 Sequence
10	230.2	48.3	513	6	AR338157	AR338157 Sequence
11	230.2	48.3	513	9	BT007182	BT007182 Homo sapi
12	230.2	48.3	513	12	BT008273	BT008273 Synthetic
13	230.2	48.3	597	9	S72960	S72960 Homo sapien
14	230.2	48.3	1744	9	BC007789	BC007789 Homo sapi
15	230.2	48.3	1759	9	BC001422	BC001422 Homo sapi
16	230.2	48.3	1780	9	BC007255	BC007255 Homo sapi
17	229.8	48.2	465	6	AR117111	AR117111 Sequence
18	229.8	48.2	465	6	AR338154	AR338154 Sequence
19	213.6	44.8	1645	6	A18411	A18411 PTGF gene s
20	213.6	44.8	1645	6	AX234464	AX234464 Sequence
21	213.6	44.8	1645	6	AX587633	AX587633 Sequence
22	213.6	44.8	1645	6	AX743110	AX743110 Sequence
23	213.2	44.7	450	6	AR117115	AR117115 Sequence
24	213.2	44.7	450	6	AR338158	AR338158 Sequence
25	213.2	44.7	450	6	BD141689	BD141689 Chimeric
26	213.2	44.7	468	6	BD141689	BD141689 Chimeric
27	203.6	42.7	229131	2	AC114701	AC114701 Rattus no
28	203.6	42.7	248529	2	AC097592	AC097592 Rattus no
29	195.6	41.0	1489	4	AB004272	AB004272 Bos tauri
30	187.6	39.3	450	6	BD141690	BD141690 Chimeric
31	176.8	37.1	167700	2	AC079735	AC079735 Mus muscu
32	176.8	37.1	274695	2	AC127582	AC127582 Mus muscu
33	147.4	30.9	474	6	BD141691	BD141691 Chimeric
34	145.4	30.5	375	4	AY157708	AY157708 Ovis arie
35	129.2	27.1	390	12	ASPLGF	Y09268 Artificial
36	121.8	25.5	474	6	BD141692	BD141692 Chimeric
37	117	24.5	203010	9	AC006530	AC006530 Homo sapi
38	116.4	24.4	495	10	GPIVEGFA	M84230 Guinea pig
39	112.8	23.6	645	4	CFAL33758	AJ133758 Canis fam
40	110.8	23.2	654	4	AF133249	AF133249 Canis fam
41	110.8	23.2	672	4	AF133250	AF133250 Canis fam
42	109.4	22.9	715	5	AB011078	AB011078 Gallus ga
43	108.8	22.8	677	6	AR272184	AR272184 Sequence
44	108.8	22.8	728	6	AR272185	AR272185 Sequence
45	108.8	22.8	3747	6	AX780130	AX780130 Sequence

ALIGNMENTS

RESULT 1	AR117110	AR117110	477 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	Sequence 38 from patent US 6140073.					
DEFINITION	Sequence 38 from patent US 6140073.					
ACCESSION	AR117110					
VERSION	AR117110.1	GI:14098016				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 477)					
AUTHORS	Bayne,M.L. and Thomas,K.A. Jr.					
TITLE	Vascular endothelial cell growth factor C subunit					
JOURNAL	Patent: US 6140073-A 38 31-OCT-2000;					
FEATURES	Location/Qualifiers					

```

source
1. .477
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 477; DB 6; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.1e-132;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCCATGAAGCTGTTCACTTGTCTTCCAGGTCTTACGCTGGTGGTGGCTGGCAC 60
|
|
|
Db 1 ATGCTGCCATGAAGCTGTTCACTTGTCTTCCAGGTCTTACGCTGGTGGTGGCTGGCAC 60
|
|
|
QY 61 TCCAGGGGCTGCTGCTGGGAAACAACCTCAACAGAAATGAAGTGGTGGCTTCAAT 120
|
|
|
Db 61 TCCAGGGGCTGCTGCTGGGAAACAACCTCAACAGAAATGAAGTGGTGGCTTCAAT 120
|
|
|
QY 121 GAAGTGTGGGCGCGAGCTACTGCGGCCAATGGAGAGCTGTGTACATGGAGTGA 180
|
|
|
Db 121 GAAGTGTGGGCGCGAGCTACTGCGGCCAATGGAGAGCTGTGTACATGGAGTGA 180
|
|
|
QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGCTCATGTGTCTTCTGAGTCGCTGTAGT 240
|
|
|
Db 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGCTCATGTGTCTTCTGAGTCGCTGTAGT 240
|
|
|
QY 241 GGTGTGTGGTGAAGGGTCTGCACTGTGTGGCGCTAAAGACAGCCAAACATCACTATG 300
|
|
|
Db 241 GGTGTGTGGTGAAGGGTCTGCACTGTGTGGCGCTAAAGACAGCCAAACATCACTATG 300
|
|
|
QY 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 360
|
|
|
Db 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 360
|
|
|
QY 361 CAGGATGTACTTCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 420
|
|
|
Db 361 CAGGATGTACTTCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 420
|
|
|
QY 421 ACCAAGGGAAGAGGAAAGCAAAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
|
|
|
Db 421 ACCAAGGGAAGAGGAAAGCAAAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
|
|
|

RESULT 2
AR338153
LOCUS 477 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 38 from patent US 5669434.
ACCESSION AR338153
VERSION AR338153.1 GI:33724885
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 477)
AUTHORS Bayne, M.L. and Thomas, K.A. Jr.
TITLE Vascular endothelial cell growth factor C subunit
JOURNAL Patent: US 5669434-A 38 27-MAY-2003;
FEATURES
Location/Qualifiers
1. .477
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 477; DB 6; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.1e-132;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCCATGAAGCTGTTCACTTGTCTTCCAGGTCTTACGCTGGTGGTGGCTGGCAC 60
|
|
|
Db 1 ATGCTGCCATGAAGCTGTTCACTTGTCTTCCAGGTCTTACGCTGGTGGTGGCTGGCAC 60
|
|
|
QY 61 TCCAGGGGCTGCTGCTGGGAAACAACCTCAACAGAAATGAAGTGGTGGCTTCAAT 120
|
|
|
Db 61 TCCAGGGGCTGCTGCTGGGAAACAACCTCAACAGAAATGAAGTGGTGGCTTCAAT 120
|
|
|
QY 121 GAAGTGTGGGCGCGAGCTACTGCGGCCAATGGAGAGCTGTGTACATGGAGTGA 180
|
|
|
Db 121 GAAGTGTGGGCGCGAGCTACTGCGGCCAATGGAGAGCTGTGTACATGGAGTGA 180
|
|
|
QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGCTCATGTGTCTTCTGAGTCGCTGTAGT 240
|
|
|
Db 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGCTCATGTGTCTTCTGAGTCGCTGTAGT 240
|
|
|
QY 241 GGTGTGTGGTGAAGGGTCTGCACTGTGTGGCGCTAAAGACAGCCAAACATCACTATG 300
|
|
|
Db 241 GGTGTGTGGTGAAGGGTCTGCACTGTGTGGCGCTAAAGACAGCCAAACATCACTATG 300
|
|
|
QY 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 360
|
|
|
Db 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 360
|
|
|
QY 361 CAGGATGTACTTCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 420
|
|
|
Db 361 CAGGATGTACTTCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 420
|
|
|
QY 421 ACCAAGGGAAGAGGAAAGCAAAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
|
|
|
Db 421 ACCAAGGGAAGAGGAAAGCAAAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
|
|
|

```

```

QY 121 GAAGTGTGGGCGCGAGCTACTGCGGCCAATGGAGAGCTGTGTACATGGAGTGA 180
|
|
|
Db 121 GAAGTGTGGGCGCGAGCTACTGCGGCCAATGGAGAGCTGTGTACATGGAGTGA 180
|
|
|
QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGCTCATGTGTCTTCTGAGTCGCTGTAGT 240
|
|
|
Db 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGCTCATGTGTCTTCTGAGTCGCTGTAGT 240
|
|
|
QY 241 GGTGTGTGGTGAAGGGTCTGCACTGTGTGGCGCTAAAGACAGCCAAACATCACTATG 300
|
|
|
Db 241 GGTGTGTGGTGAAGGGTCTGCACTGTGTGGCGCTAAAGACAGCCAAACATCACTATG 300
|
|
|
QY 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 360
|
|
|
Db 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 360
|
|
|
QY 361 CAGGATGTACTTCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 420
|
|
|
Db 361 CAGGATGTACTTCCGCAATCGGATCCACATTCCTTACGTGAGATGACATTTCTCT 420
|
|
|
QY 421 ACCAAGGGAAGAGGAAAGCAAAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
|
|
|
Db 421 ACCAAGGGAAGAGGAAAGCAAAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
|
|
|

RESULT 3
RATPLGF 665 bp mRNA linear ROD 17-APR-1996
LOCUS Ratrus norvegicus placenta growth factor (PIGF) mRNA, complete cds.
DEFINITION L40030
ACCESSION L40030.1 GI:1263413
VERSION Rattus norvegicus (Norway rat)
KEYWORDS angiogenesis; growth factor.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 665)
AUTHORS DiSalvo, J., Bayne, M.L., Conn, G., Kwok, P.W., Trivedi, P.G.,
Soderman, D., Palisi, T.M., Sullivan, K.A. and Thomas, K.A.
TITLE Purification and characterization of a naturally occurring vascular
endothelial growth factor: placenta growth factor heterodimer
J. Biol. Chem. 270 (13), 7717-7723 (1995)
MEDLINE 95221439
PUBMED 7706320
COMMENT Original source text: Rattus norvegicus cDNA to mRNA.
FEATURES
Location/Qualifiers
1. .665
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/cell_line="GS-9L"
1. .665
/gene="PIGF"
<1. .>665
/gene="PIGF"
<1. .>39
/gene="PIGF"
40. 516
/gene="PIGF"
/codon_start=1
/product="placenta growth factor"
/protein_id="AAA97426.1"
/db_xref="GI:1263414"
/translation="MLANKLFTCEQLQVLAVHSGALSGNNSSTEMBWPPEVWVG
RSCYRPMKLVYIADEHNEVSHIFSPCVLLSRGCGGDLGHLVAKTANITWQI
LKIPNRDPHSYVEMTFSDVLCRPILETTKAERKTKGRKKSKEFTQTEPHL"
517. .>665
/gene="PIGF"
3' UTR
ORIGIN
Query Match 99.7%; Score 475.4; DB 10; Length 665;

```



```

Best Local Similarity 99.8%; Pred. No. 1.6e-131;
Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGCCATGAAGCTGTTCACTGCTTCTTGCGAGTCTCTAGCTGGTGGCTGTGCAC 60
Db 40 ATGCTGCCATGAAGCTGTTCACTGCTTCTTGCGAGTCTCTAGCTGGTGGCTGTGCAC 99
QY 61 TCCAGGGGGCCCTGCTGCTGGGAAACAACCTCAACAGAAATGGAAGTGGTGCCTTTCAAT 120
Db 100 TCCAGGGGGCCCTGCTGCTGGGAAACAACCTCAACAGAAATGGAAGTGGTGCCTTTCAAT 159
QY 121 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGAGAGAGCTGGTGTACATTCAGATGAA 180
Db 160 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGAGAGAGCTGGTGTACATTCAGATGAA 219
QY 181 CACCCTAAATGAAGTGTCTCATATATTCAGTCCGTCATGTGCTTCTGAGTTCGCTGTAGT 240
Db 220 CACCCTAAATGAAGTGTCTCATATATTCAGTCCGTCATGTGCTTCTGAGTTCGCTGTAGT 279
QY 241 GGCTGCTGTGGTGAACGAGGCTCTGCACTGTGTGGCGCTAAAGACAGCAACATCACTATG 300
Db 280 GGCTGCTGTGGTGAACGAGGCTCTGCACTGTGTGGCGCTAAAGACAGCAACATCACTATG 339
QY 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTACGTGGAGATGACATTTCT 360
Db 340 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTACGTGGAGATGACATTTCT 399
QY 361 CAGGATGTACTTCGGAATCAGGCTTCTTCTGGAGACGACAAAGGAGAGAGGAGAA 420
Db 400 CAGGATGTACTTCGGAATCAGGCTTCTTCTGGAGACGACAAAGGAGAGAGGAGAA 459
QY 421 ACCAAGGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
Db 460 ACCAAGGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516

RESULT 4
MMP1GF 1370 bp mRNA linear ROD 26-DEC-1999
LOCUS Mus musculus mRNA for placenta growth factor (PLGF gene).
DEFINITION X80171
ACCESSION X80171.1 GI:1063401
VERSION placenta growth factor; PLGF; PLGF-2 protein.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1370)
Dipalma.T., Tucci.M., Russo.G., Maglione.D., Lago.C.T., Romano.A.,
Sacccone.S., Della Valle.G., De Gregorio.L., Dragani.T.A.,
Viglietto.G. and Persico.M.G.
The placenta growth factor gene of the mouse
Mamm. Genome 7 (1), 6-12 (1996)
97059399
MEDLINE 8903720
PUBMED
REFERENCE 2 (bases 1 to 1370)
AUTHORS Persico, M.G.
DIRECT SUBMISSION
TITLE Submitted (14-JUN-1994) M.G. Persico, International Institute of,
JOURNAL Genetics and Biophysics, Via G Marconi 12, 80125 Naples, ITALY
FEATURES
source
1. .1370
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="heart"
/clone_lib="mouse heart cDNA"
/dev_stage="adult"
119..595
/gene="PLGF"
119..595
CDS
/gene="PLGF"
/codon_start=1

```

```

/product="placenta growth factor"
/protein_id="CAA56453.1"
/db_xref="GI:1063402"
/db_xref="GOA:P49764"
/db_xref="SWISS-PROT:P49764"
/translation="MLVIMKLFCTFLQVLAVHSQALSAGNNSTEVEVVPFNEVWG
RSCRMELKVIILDEYDEVSHIFSPSCVLLSRCSCGDEGLHCVPIKANTIMQI
LKIPPRNDPHFYVEMTFSQDLCECRPILLETTKARRKTKRKRKRSNSTEHP"
1342..1347
/gene="PLGF gene"
1342..1347
/gene="PLGF gene"

polyA_site
ORIGIN
Query Match 87.9%; Score 419.4; DB 10; Length 1370;
Best Local Similarity 92.5%; Pred. No. 1.1e-114;
Matches 441; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGCTGCCATGAAGCTGTTCACTGCTTCTTGCGAGTCTCTAGCTGGTGGCTGTGCAC 60
Db 119 ATGCTGCCATGAAGCTGTTCACTGCTTCTTGCGAGTCTCTAGCTGGTGGCTGTGCAT 178
QY 61 TCCAGGGGGCCCTGCTGCTGGGAAACAACCTCAACAGAAATGGAAGTGGTGCCTTTCAAT 120
Db 179 TCCAGGGGGCCCTGCTGCTGGGAAACAACCTCAACAGAGTGGTGGTGCCTTTCAAC 238
QY 121 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGAGAGAGCTGGTGTACATTCAGATGAA 180
Db 239 GAAGTGTGGGGTGGAGCTACTGCGGCCAATGAGAGAGCTGGTGTACATTCAGATGAA 298
QY 181 CAGCTTAATGAAGTGTCTCATATATTCAGTCCGTCATGTGCTTCTGAGTTCGCTGTAGT 240
Db 299 TACCCCGATGAGGTGTCTCATATATTCAGTCCGTCCTGCTTCTGAGTTCGCTGTAGT 358
QY 241 GGCTGCTGTGGTGAAGGCTCTGCACTGTGTGGCGCTAAAGACAGCAACATCACTATG 300
Db 359 GGCTGCTGTGGTGAAGGCTCTGCACTGTGTGGCGCTAAAGACAGCAACATCACTATG 418
QY 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTACGTGGAGATGACATTTCT 360
Db 419 CAGATCTTGAAGATTCCTCCCAATCGGATCCACATTTCTATGTGGAGATGACATTTCT 478
QY 361 CAGGATGTACTTCGGAATGAGGCTTCTTGAGACGACAAAGGAGAGAGAGAGAGAGAG 420
Db 479 CAGGATGTCTGTGAATGAGACCTATTCTTGAGACGACAAAGGAGAGAGAGAGAGAG 538
QY 421 ACCAAGGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
Db 539 ACCAAGGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595

RESULT 5
MMPGF 1580 bp mRNA linear ROD 21-AUG-1996
LOCUS M.musculus mRNA for placenta growth factor.
DEFINITION X96793
ACCESSION X96793.1 GI:1502350
VERSION placenta growth factor.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Achen, M.G., Gad, J.M., Stacker, S.A. and Wilks, A.F.
Placenta growth factor and vascular endothelial growth factor are
co-expressed during early embryonic development
Unpublished
REFERENCE 2 (bases 1 to 1580)
AUTHORS Achen, M.G.
DIRECT SUBMISSION
TITLE Submitted (22-MAR-1996) M.G. Achen, Ludwig Institute for Cancer
JOURNAL Research, Melbourne Branch, Post Office Box 2008, Royal Melbourne
Hospital, Victoria 3050, Australia

```

FEATURES		Location/Qualifiers	
source	1..1580	/organism="Mus musculus"	
		/mol_type="mRNA"	
CDS	318..794	/strain="NIH Swiss"	
		/db_xref="taxon:10090"	
CDS	318..794	/dev_stage="10 days post-coital embryo"	
		/codon_start=1	
ORIGIN	Query Match	/product="placenta growth factor"	
	Best Local Similarity 92.5%; Score 419.4; DB 10; Length 1580;	/protein_id="CA65587.1"	
ORIGIN	Matches 441; Conservative 0; Mismatches 36; Indels 0; Gaps 0;	/db_xref="GI:1502351"	
		/db_xref="GOA:P49764"	
ORIGIN	1 ATGCTGGCATGAAGCTGTTCACCTGCTTTCGAGTCTAGCTGGTGGCTGGTGGAC 60	/translation="MLVMTKFTCFLOVLAVHSGALNSAGNNSSTEVVPPNEVWG	
	318 ATGCTGGTGTGATGAAGCTGTTCACCTGCTTTCGAGTCTAGCTGGTGGCTGGCAT 377	RSYCRMEKLVIIDYVDESHIFSPSCVLLSRCSGCCGDLGHCVPKTKANITMQI	
ORIGIN	61 TCCAGGGGCGCTGTCTGTGGGAACAACCTCAACAGAAATGGAAGTGGTGCCTTTCAAT 120	LKIPNDRDFHYVEMTFSDVLCRPILETTKAERRTKGKRKRNSQTEBPH"	
	378 TCCAGGGGCGCTGTCTGTGGGAACAACCTCAACAGAAATGGAAGTGGTGCCTTTCAAC 437		
ORIGIN	121 GAAGTGTGGGGCGCGAGCTACTCCGCCCAATGGAGAACTGGTGTACATTCGAGATGAA 180		
	438 GAAGTGTGGGGCGCGAGCTACTCCGCCCAATGGAGAACTGGTGTACATTCGAGATGAA 497		
ORIGIN	181 CACCTTAAGTGTCTCATATATTTCAGTCCGTATGTCCTTCTGAGTGCCTGTAGT 240		
	498 TACCTCTGATGAGTGTCTCATATATTTCAGTCCGTATGTCCTTCTGAGTGCCTGTAGT 557		
ORIGIN	241 GGCTGTGTGGTGCAGAGGGTGTGCACTGTGTGGCGCTAAAGACAGCCCAACATCATATG 300		
	558 GGCTGTGTGGTGTGAGAGTGTGCACTGTGTGCCAATAAGACACCAACATCATATG 617		
ORIGIN	301 CAGATCTTAAAGATTCCTCCCAATCGGATGCCATTCCTACGTGGAGATGACATTTCT 360		
	618 CAGATCTTGAAGATTCCTCCCAATCGGATGCCATTCCTACGTGGAGATGACATTTCT 677		
ORIGIN	361 CAGGATGTACTCTGCAATGCAGGCTTATCTGGACAGCAACAGCAGAGGAGGAGAA 420		
	678 CAGGATGTCTGTGAAATGCAGACCTATTTCTGGAGACGACAAAGGACAGAGGAGGAA 737		
ORIGIN	421 ACCAAGGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477		
	738 ACCAAGGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 794		
RESULT 6		1674 bp mRNA linear ROD 03-OCT-2003	
BC016567		Mus musculus placental growth factor, mRNA (cdna clone MGC:11485	
LOCUS		IMAGE:2649577), complete cds.	
DEFINITION		BC016567	
ACCESSION		MGC.	
VERSION		Mus musculus (house mouse)	
KEYWORDS		Mus musculus	
SOURCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
ORGANISM		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE		1 (bases 1 to 1674)	
AUTHORS		Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,	
		Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,	
		Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,	
		Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,	

FEATURES		Location/Qualifiers	
source	1..1674	/organism="Mus musculus"	
		/mol_type="mRNA"	
CDS	323..799	/strain="129, C57BL/6J, FVB/N"	
		/db_xref="taxon:10090"	
CDS	323..799	/clone="MGC:11485 IMAGE:2649577"	
		/tissue_type="Mammary tumor. Brca1-/fl; MMTV-Cre model. 10	
CDS	323..799	/months_old, gross tissue."	
		/clone_lib="NCI CGAP Mam3"	
CDS	323..799	/lab_host="DH10B"	
		/note="Vector: pCMV-SPORT6"	
CDS	323..799	/gene="Pgfn"	
		/note="synonym: Plgfn"	
CDS	323..799	/db_xref="LocusID:18654"	
		/db_xref="MGI:105095"	
CDS	323..799	/codon_start=1	
		/product="placental growth factor"	
CDS	323..799	/protein_id="ASH16567.1"	
		/db_xref="GI:16741507"	
CDS	323..799	/db_xref="LocusID:18654"	
		/translation="MLVMTKFTCFLOVLAVHSGALNSAGNNSSTEVVPPNEVWG	
CDS	323..799	RSYCRMEKLVIIDYVDESHIFSPSCVLLSRCSGCCGDLGHCVPKTKANITMQI	
		LKIPNDRDFHYVEMTFSDVLCRPILETTKAERRTKGKRKRNSQTEBPH"	

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shvchenko, Y.,
 Sanchez, A., Whiting, M., Touchman, J.W., Green, E.D.,
 Bouffard, G.G., Blakesley, R.W., Grimwood, J., Schmutz, J., Myers, R.M.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 12477932
 2 (bases 1 to 1674)
 PubMed
 Direct Submission
 Strausberg, R.
 Submitted (31-OCT-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: gcapbs@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lousseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAC plate: 16 Row: a Column: 3
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 6679288.
 Location/Qualifiers
 1..1674
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129, C57BL/6J, FVB/N"
 /db_xref="taxon:10090"
 /clone="MGC:11485 IMAGE:2649577"
 /tissue_type="Mammary tumor. Brca1-/fl; MMTV-Cre model. 10
 months old, gross tissue."
 /clone_lib="NCI CGAP Mam3"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 1..1674
 /gene="Pgfn"
 /note="synonym: Plgfn"
 /db_xref="LocusID:18654"
 /db_xref="MGI:105095"
 323..799
 /codon_start=1
 /product="placental growth factor"
 /protein_id="ASH16567.1"
 /db_xref="GI:16741507"
 /db_xref="LocusID:18654"
 /translation="MLVMTKFTCFLOVLAVHSGALNSAGNNSSTEVVPPNEVWG
 RSYCRMEKLVIIDYVDESHIFSPSCVLLSRCSGCCGDLGHCVPKTKANITMQI
 LKIPNDRDFHYVEMTFSDVLCRPILETTKAERRTKGKRKRNSQTEBPH"
 458..709
 misc_feature

FEATURES	source	Location/Qualifiers
ORIGIN		1. .513 /organism="unknown" /mol_type="genomic DNA"
Query Match		48.3%; Score 230.2; DB 6; Length 513;
Best Local Similarity		71.6%; Pred. No. 7.4e-58;
Matches 336; Conservative		0; Mismatches 118; Indels 15; Gaps 2;
QY		1 ATGCTGGCCATGAAGCTGTTCACCTTCTCTTGACAGGTCCCTAGCTGGGTGTGCTGTGCAC 60
Db		
QY		1 ATGCGGTTCATGAGGCTGTTCCTTGTCTCTGAGCTCCTGCCGGCTGCGCTGCCT 60
Db		
QY		61 TCC-----CAGGGGCCCTGTCTGCTGGGAACAATCAACAGAAATGGAAGTG 108
Db		
QY		61 GCTGTGCCCCCAGCAGTGGGCCCTTGTCTGCTGGGAACGGCTCGTCAGAGGTGGAAGTG 120
Db		
QY		109 GTGCTTTCAATGAAGTGTGGGGCGCAGCTACTCCGCCCAATCGAGAGAGCTGTGTATC 168
Db		
QY		121 GTACCTTCCAGAGTGTGGGGCGCAGCTACTGCGGGCGCTGGAGAGCTGTGTGAC 180
Db		
QY		169 ATTGCAGATGAACCCCTAATGAAGTGTCTCATATATTCAAGTCCGTATGTCTCTTCTG 228
Db		
QY		181 GTCTGTGTCGAGTACCCAGCGAGGTGGAGCACATGTTCAAGCCATCTGTGTCTCCCTG 240
Db		
QY		229 AGTCGCTGTAGTGGCTGTGTGTCACAGAGGTCTGCACCTGTGTGGCCTTAAGACAGCC 288
Db		
QY		241 CTGCGCTGCACGGTGTGTGCGGCGATGAGAACTGCACTGTGTCCCGTGGAGACGGCC 300
Db		
QY		289 AACATCACTATGCAGATCTTAAAGATCCCCCAATCGGGATCCACATTCCTACCTGGAG 348
Db		
QY		301 AATGTCACCATGCASCTCTTAAGAT---CCGTTCTGGGACCGGCCCTCTACGTGGAG 357
Db		
QY		349 ATGACATTTCTCAGGATGTACTCTGCGAATGCAGGCTATTCTGGAGACGACAAAGCA 408
Db		
QY		358 CTGACGTTCTCTCAGCAGCTTCTGTGCGAATGCCGGCTCTGCGGGAGAAATGAAGCG 417
Db		
QY		409 GAAAGGAGGAAACCAAGGGAGAGGAAGCAAGCAAAACCCACAGA 457
Db		
QY		418 GAAAGGAGGAGACCCAGCGGAGGGGAGAGGAGAGAGACAGACAGA 466
Db		
RESULT 11		
BT007182		513 bp mRNA linear PRI 13-MAY-2003
LOCUS		Hom sapiens placental growth factor, vascular endothelial growth
DEFINITION		factor-related protein mRNA, complete cds.
ACCESSION		BT007182
VERSION		BT007182.1 GI:30583202
KEYWORDS		FLI CDNA.
SOURCE		Hom sapiens (human)
ORGANISM		Hom sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		1 (bases 1 to 513)
		Kalinine,N., Chen,X., Rolfs,A., Halleck,A., Hines,I., Eisenstein,S.,
		Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
		Pheilan,M. and Farmer,A.
TITLE		Cloning of human full-length CDSs in BD Creator (TM) System Donor
		vector
JOURNAL		Unpublished
REFERENCE		2 (bases 1 to 513)
AUTHORS		Kalinine,N., Chen,X., Rolfs,A., Halleck,A., Hines,I., Eisenstein,S.,
		Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
		Pheilan,M. and Farmer,A.
TITLE		Direct Submission
JOURNAL		Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
		Circle, Palo Alto, CA 94303, USA
COMMENT		This CDS clone is a part of a collection of human full length
		expression clones generated by BD Biosciences Clontech and the
		Harvard Institute of Proteomics. Each CDS has been cloned in two
		forms: with and without stop-codon (to allow fusion with C-terminal

tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: <http://bioinfo.clontech.com/orfclones>.

FEATURES

Location/Qualifiers
1..513
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GH00781X1.0"
/clone_lib="BD Creator (TM) CDS Library derived from MGC collection"
/lab_host="DH5alpha T1 resistant"
/note="vector: pDNR-Dual"
1..513
/codon_start=1
/product="placental growth factor, vascular endothelial growth factor-related protein"
/protein_id="AAP35846.1"
/db_xref="GI:305853203"
/translation="MPVMRLFPDCLQLLAGLPAVPPQWALSAGNSSEVVPFQ EWMGRSYCRALERLVDVSVSEVSEHMFSPCVSLRCTGCCDENLHCVPTANV TMLLKRSGDRPSYVELTFSQVRCRPLREKMPERRPKGRKRREKQRTDC HLCGDVPRRL"

ORIGIN

Query Match 48.3%; Score 230.2; DB 9; Length 513;
Best Local Similarity 71.6%; Pred. No. 7.4e-58;
Matches 336; Conservative 0; Mismatches 118; Indels 15; Gaps 2;
QY 1 ATGCTGCCATGAGCTGTTACCTTCTTCTGAGCTCTCTAGCTGGTGGTGGTGCAC 60
DB 1 ATGCGGTGATGAGCTGTTCCCTTGTCTCTGAGCTCTCTGGCGGGCTGGCTGCT 60
QY 61 TCC-----CAGGGGGCCCTGTCTGCTGGGAACAACTCAACAGAAATGGAAGTG 108
DB 61 GCTGTGCCCCCAGCAGTGGCCCTTGTCTGCTGGGAAGGCTCTGTGAGAGTGAAGTG 120
QY 109 GTGCTTTCAATGAAGTGTGGGCGGAGCTACTGCGCGCAATGGAGAAGCTGGTGTAC 168
DB 121 GTACCTTCCAGGAAGTGTGGGCGGAGCTACTGCGGGCGCTGGAGAGCTGGTGAC 180
QY 169 ATTCAGATGAACCCCTAATGAAGTGTCTATATTTACGTCCGTCTATGTCTCTTG 228
DB 181 GTGTGTCGAGTACCCAGCGAGTGGAGCAGATGTTACCCCATCTGTCTCTCTG 240
QY 229 AGTCGCTGTAGTGGCTGTGTGTGACGAGGCTCTGCACTGTGTGGCTAAAGACGCC 288
DB 241 CTGGCTGCACCGCTGTGCGGATGAGATCTGCACTGTGTGCGGTGAGACGGCC 300
QY 289 AACATCACTATGAGATTTAAAGATTCCGCCCAATCGGATCCATCTCTAGTGGAG 348
DB 301 AATGTCACTATGAGTCTCTAAAGAT---CGTTTCTGGGACCGCCCTCTCTAGTGGAG 357
QY 349 ATGACATCTCTCAGATGTACTCTGCAATGCGAGCTTATCTGGAGACCAAGGCA 408
DB 358 CTGAGTCTCTCAGCAGTGTCTGTCGAATGCGCGCTCTGCGGGAAGATGAAGCCG 417
QY 409 GAAAGGAGGAAACCAAGGGGAAGAGGAGCAAGCAAAACCCACACAGA 457
DB 418 GAAAGGAGGAGACCAAGGCGAGGGGAAGAGGAGAGAGAGAGACAGA 466

RESULT 12
BT008273

LOCUS BT008273 513 bp mRNA linear SYN 13-MAY-2003
DEFINITION Synthetic construct Homo sapiens placental growth factor, vascular endothelial growth factor-related protein mRNA, partial cds.

ACCESSION BT008273
VERSION BT008273.1 GI:30585384
KEYWORDS FLI_CDNA.

SOURCE

ORGANISM

synthetic construct

artificial sequences

1 (bases 1 to 513)

REFERENCE

AUTHORS

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A.

TITLE

JOURNAL

REFERENCE

AUTHORS

Phelan,M. and Farmer,A.

TITLE

JOURNAL

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

COMMENT

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: <http://bioinfo.clontech.com/orfclones>.

FEATURES

source

1..513
/organism="synthetic construct"

/mol_type="mRNA"

/db_xref="taxon:32630"

/clone="GH00781X1.0"

/clone_lib="BD Creator (TM) CDS Library derived from MGC collection"

/lab_host="DH5alpha T1 resistant"

/note="vector: pDNR-Dual"

1..513

/note="Mutations: 512:Stop->Leu"

/codon_start=1

/transl_table=11

/product="Homo sapiens placental growth factor, vascular endothelial growth factor-related protein"

/protein_id="AAP36965.1"

/db_xref="GI:30585385"

/translation="MPVMRLFPDCLQLLAGLPAVPPQWALSAGNSSEVVPFQ EWMGRSYCRALERLVDVSVSEVSEHMFSPCVSLRCTGCCDENLHCVPTANV TMLLKRSGDRPSYVELTFSQVRCRPLREKMPERRPKGRKRREKQRTDC HLCGDVPRRL"

ORIGIN

Query Match 48.3%; Score 230.2; DB 12; Length 513;
Best Local Similarity 71.6%; Pred. No. 7.4e-58;
Matches 336; Conservative 0; Mismatches 118; Indels 15; Gaps 2;
QY 1 ATGCTGCCATGAGCTGTTACCTTCTTCTGAGCTCTCTAGCTGGTGGTGGTGCAC 60
DB 1 ATGCGGTGATGAGCTGTTCCCTTGTCTCTGAGCTCTCTGGCGGGCTGGCTGCT 60
QY 61 TCC-----CAGGGGGCCCTGTCTGCTGGGAACAACTCAACAGAAATGGAAGTG 108
DB 61 GCTGTGCCCCCAGCAGTGGCCCTTGTCTGCTGGGAAGGCTCTGTGAGAGTGAAGTG 120
QY 109 GTGCTTTCAATGAAGTGTGGGCGGAGCTACTGCGCGCAATGGAGAAGCTGGTGTAC 168
DB 121 GTACCTTCCAGGAAGTGTGGGCGGAGCTACTGCGGGCGCTGGAGAGCTGGTGAC 180
QY 169 ATTCAGATGAACCCCTAATGAAGTGTCTATATTTACGTCCGTCTATGTCTCTTG 228
DB 181 GTGTGTCGAGTACCCAGCGAGTGGAGCAGATGTTACCCCATCTGTCTCTCTG 240
QY 229 AGTCGCTGTAGTGGCTGTGTGTGACGAGGCTCTGCACTGTGTGGCTAAAGACGCC 288

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 19:32:13 ; Search time 307 Seconds
(without alignments)

6600.620 Million cell updates/sec

Title: US-10-071-370A-3

Perfect score: 477

Sequence: 1 atgtcgccatgaagctgtt.....ctgaggaaacccacctgtga 477

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N_Geneseq_29Jan04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001as:*
 - 5: Geneseq2001bs:*
 - 6: Geneseq2002s:*
 - 7: Geneseq2003as:*
 - 8: Geneseq2003bs:*
 - 9: Geneseq2003cs:*
 - 10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	477	100.0	477	2	AAQ28956	AaQ28956 Sequence
2	477	100.0	477	3	AAZ39830	AaZ39830 VEGF 158
3	477	100.0	477	4	AAC83515	AaC83515 Rat VEGF
4	477	100.0	477	8	ADA25600	Ada25600 Rat cDNA
5	475.4	99.7	477	2	AAQ28952	AaQ28952 Sequence
6	475.4	99.7	477	2	AAQ23040	AaQ23040 Encodes V
7	475.4	99.7	477	2	AAV25538	AaV25538 Vascular
8	475.4	99.7	477	2	AAV25536	AaV25536 Vascular
9	475.4	99.7	477	4	AAF81273	AaF81273 cDNA enco
10	475.4	99.7	477	4	AAF81272	AaF81272 Rat VEGF
11	475.4	99.7	477	7	ACA62374	AcA62374 cDNA enco
12	475.4	99.7	477	7	ACA62371	AcA62371 cDNA enco
13	414	86.8	417	2	AAQ28955	AaQ28955 Sequence
14	414	86.8	417	3	AAZ39829	AaZ39829 VEGF 138
15	414	86.8	417	4	AAC83514	AaC83514 Rat VEGF
16	414	86.8	417	8	ADA25598	Ada25598 Rat cDNA
17	412.4	86.5	417	2	AAQ23041	AaQ23041 Encodes V
18	412.4	86.5	417	2	AAV25537	AaV25537 Vascular
19	412.4	86.5	417	4	AAF81274	AaF81274 cDNA enco
20	412.4	86.5	417	7	ACA62375	AcA62375 cDNA enco
21	412.4	86.5	417	7	ACA62372	AcA62372 cDNA enco
22	396.4	83.1	423	2	AAV25539	AaV25539 Vascular
23	230.2	48.3	513	3	AAZ39801	AaZ39801 Vascular

24	230.2	48.3	513	4	AAC83519	AaC83519 Human VEG
25	230.2	48.3	513	8	ADA25606	Ada25606 Rat cDNA
26	230.2	48.3	597	4	AAA91000	Aaa91000 Human PIG
27	229.8	48.2	465	2	AAQ28948	AaQ28948 Sequence
28	229.8	48.2	465	3	AAZ39831	AaZ39831 VEGF 154
29	229.8	48.2	465	4	AAC83516	AaC83516 Rat VEGF
30	229.8	48.2	465	8	ADA25602	Ada25602 Rat cDNA
31	213.6	44.8	1645	4	AAA90999	Aaa90999 Human PIG
32	213.6	44.8	1645	4	AAAS12876	AaAS12876 DNA enco
33	213.6	44.8	1645	6	ABZ35479	AbZ35479 Human gen
34	213.6	44.8	1645	6	ABV94112	AbV94112 Breast ca
35	213.6	44.8	1645	6	ABK84573	AbK84573 Human cDN
36	213.6	44.8	1645	7	ABX08796	AbX08796 Angiogene
37	213.6	44.8	1645	9	ADD08951	Add08951 Human PIG
38	213.2	44.7	450	3	AAZ39834	AaZ39834 VEGF 149
39	213.2	44.7	450	4	AAC83520	AaC83520 Human VEG
40	213.2	44.7	450	8	ADA25608	Ada25608 Rat cDNA
41	213.2	44.7	468	5	ABL50280	AbL50280 Chimeric
42	210.4	44.1	1645	2	AAQ24268	AaQ24268 Encodes P
43	187.6	39.3	450	6	ABL50281	AbL50281 Human PIG
44	168.4	35.3	475	8	ACH14601	ACH14601 Human adu
45	147.4	30.9	474	6	ABL50282	AbL50282 Human PIG

ALIGNMENTS

RESULT 1
AAQ28956
ID AAQ28956 standard; cDNA; 477 BP.

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

XX AC AAQ28956;

CC single band migrating at 108 bp was gel purified, digested with Sall,
CC ligated into pGEM3zf(+) and sequenced. The nucleotide sequence obtained
CC (pYG) was used to design antisense and sense PCR primers to amplify the
CC 5' and 3' ends of the cDNA. These 5' and 3' clones are denoted p5V2 and
CC p3V2 respectively. The entire base sequence for the 158 amino acid
CC microheterogeneous B subunit and the 138 amino acid microheterogeneous
CC subunit are shown in AAQ28955 and AAQ28956. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)
XX
SQ Sequence 477 BP; 123 A; 116 C; 133 G; 105 T; 0 U; 0 Other;

Query Match 100.0%; Score 477; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 4.1e-133;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGCCATGAAGCTGTTCACCTGCTTCTTGCAGGTCTAGCTGGTTGGCTGTGCAC 60
Db 1 ATGCTGCCATGAAGCTGTTCACCTGCTTCTTGCAGGTCTAGCTGGTTGGCTGTGCAC 60
QY 61 TCCAGGGGCGCTGTCTGTGGGAACTCACTCAACAGAAATGGAAGTGGCTTTCAAT 120
Db 61 TCCAGGGGCGCTGTCTGTGGGAACTCACTCAACAGAAATGGAAGTGGCTTTCAAT 120
QY 121 GAAGTGTGGGCGCGAGCTACTCCGCGCAATGGAGAGCTGTGTACATTGAGATGAA 180
Db 121 GAAGTGTGGGCGCGAGCTACTCCGCGCAATGGAGAGCTGTGTACATTGAGATGAA 180
QY 181 CACCCTAATGAAGTGTCTCATATATTCACTCCGCTCATGTCTTCTGAGTCCGTGTAGT 240
Db 181 CACCCTAATGAAGTGTCTCATATATTCACTCCGCTCATGTCTTCTGAGTCCGTGTAGT 240
QY 241 GGCTGTGTGTGACGAGGCTGTGCTGTGGCGCTAAAGACAGCCACATCACTATG 300
Db 241 GGCTGTGTGTGACGAGGCTGTGCTGTGGCGCTAAAGACAGCCACATCACTATG 300
QY 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTACCTGGAGATGACATTTCT 360
Db 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTACCTGGAGATGACATTTCT 360
QY 361 CAGGATGTACTTCCGAATCAGGCTTATTTCTGGAGACGACAAAGGAGGAGGAAA 420
Db 361 CAGGATGTACTTCCGAATCAGGCTTATTTCTGGAGACGACAAAGGAGGAGGAAA 420
QY 421 ACCAAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
Db 421 ACCAAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477

RESULT 2
ID AA239830 standard; cDNA; 477 BP.
XX
AC AA239830;
XX
DT 15-FEB-2000 (first entry)
XX
DE VEGFB 158 amino acid residue subunit nucleotide sequence.
XX
KW VEGF, vascular endothelial growth factor; B subunit; tissue growth;
KW vascular development; artificial blood vessel; repair; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .477
FT /tag= a
FT /product= "VEGFB"
FT /note= "158 amino acid residue subunit"
XX

US5994300-A.
XX
XX
XX 30-NOV-1999.
XX

PF 20-SEP-1993; 93US-00124259.
XX
PR 28-MAR-1991; 91US-00676436.
XX
PA (MERI) MERCK & CO INC.
XX
PI Thomas KA, Bayne ML;
XX
DR WPI; 2000-038268/03.
XX
P-PSDB; AAY57032.
XX
PT Purified and isolated vascular endothelial cell growth factor C subunit
PT for the induction of tissue repair or growth.
XX
PS Disclosure; Fig 8; 58pp; English.
XX
CC This is the nucleotide sequence of a 158 amino acid residue B subunit of
CC vascular endothelial cell growth factor (VEGF). The invention relates to
CC a purified and isolated VEGF C subunit amino acid sequence AAY57025. VEGF
CC exists in various microheterogeneous forms, and is useful for the
CC promotion of vascular development and repair. The invention also relates
CC to human VEGF heterodimers AC or BC and homodimer CC, where A, B and C
CC are subunit amino acid sequences. The VEGF AC, BC or CC amino acid
CC sequences can be used in a tissue repairing pharmaceutical composition.
CC The novel growth factors are useful for the production or coverage of
CC artificial blood vessels with vascular endothelial cell. They are also
CC useful for the induction of tissue growth and repair
XX
SQ Sequence 477 BP; 123 A; 116 C; 133 G; 105 T; 0 U; 0 Other;

Query Match 100.0%; Score 477; DB 3; Length 477;
Best Local Similarity 100.0%; Pred. No. 4.1e-133;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGCCATGAAGCTGTTCACCTGCTTCTTGCAGGTCTAGCTGGTTGGCTGTGCAC 60
Db 1 ATGCTGCCATGAAGCTGTTCACCTGCTTCTTGCAGGTCTAGCTGGTTGGCTGTGCAC 60
QY 61 TCCAGGGGCGCTGTCTGTGGGAACTCACTCAACAGAAATGGAAGTGGCTTTCAAT 120
Db 61 TCCAGGGGCGCTGTCTGTGGGAACTCACTCAACAGAAATGGAAGTGGCTTTCAAT 120
QY 121 GAAGTGTGGGCGCGAGCTACTCCGCGCAATGGAGAGCTGTGTACATTGAGATGAA 180
Db 121 GAAGTGTGGGCGCGAGCTACTCCGCGCAATGGAGAGCTGTGTACATTGAGATGAA 180
QY 181 CACCCTAATGAAGTGTCTCATATATTCACTCCGCTCATGTCTTCTGAGTCCGTGTAGT 240
Db 181 CACCCTAATGAAGTGTCTCATATATTCACTCCGCTCATGTCTTCTGAGTCCGTGTAGT 240
QY 241 GGCTGTGTGTGACGAGGCTGTGCTGTGGCGCTAAAGACAGCCACATCACTATG 300
Db 241 GGCTGTGTGTGACGAGGCTGTGCTGTGGCGCTAAAGACAGCCACATCACTATG 300
QY 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTACCTGGAGATGACATTTCT 360
Db 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTACCTGGAGATGACATTTCT 360
QY 361 CAGGATGTACTTCCGAATCAGGCTTATTTCTGGAGACGACAAAGGAGGAGGAGGAG 420
Db 361 CAGGATGTACTTCCGAATCAGGCTTATTTCTGGAGACGACAAAGGAGGAGGAGGAG 420
QY 421 ACCAAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
Db 421 ACCAAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477

RESULT 3
AAC83515
ID AAC83515 standard; cDNA; 477 BP.
XX
AC AAC83515;
XX

DT 25-FEB-2001 (first entry)
XX Rat VEGF subunit B coding sequence SEQ ID NO: 38.
DE Vascular endothelial growth factor; VEGF C subunit; cell division;
XX artificial blood vessel; tissue growth; tissue repair; ss.
KW Rattus sp.
XX
XX US6140073-A.
XX 31-OCT-2000.
XX 16-JAN-1996; 96US-00586039.
XX 28-MAR-1991; 91US-00676436.
XX 20-SEP-1993; 93US-00124259.
XX (MERI) MERCK & CO INC.
XX Thomas KA, Bayne ML;
XX WPI; 2001-014858/02.
XX P-PSDB; AAB37508.
XX Human vascular endothelial cell growth factor (VEGF) C subunit DNA and
XX protein, useful for promoting vascular development and repair, and for
XX promoting tissue repair, especially for treating wounds in mammals.
XX Example 10; Fig 8; 58pp; English.
XX The present invention is concerned with the human vascular endothelial
XX growth factor (VEGF) C subunit. VEGF is a vascular endothelial cell
XX mitogen and can be used to promote vascular development and repair. The C
XX subunit may exist as a homodimer or a heterodimer with the VEGF A or B
XX subunit. VEGF can be used in the treatment of wounds of mammals, to cover
XX artificial blood vessels with vascular endothelial cells, in the
XX production of artificial blood vessels and to induce tissue repair or
XX growth
XX
XX SQ Sequence 477 BP; 123 A; 116 C; 133 G; 105 T; 0 U; 0 Other;
Query Match 100.0%; Score 477; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 4.le-133;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGGCCATGAAGCTGTTCACTGCTTCTTGTGAGTCTCTAGCTGGTGGCTGTGCAC 60
Db 1 ATGCTGGCCATGAAGCTGTTCACTGCTTCTTGTGAGTCTCTAGCTGGTGGCTGTGCAC 60
Qy 61 TCCAGAGGGGGCCCTGCTGCTGGGAACAACCTCAACAGAAATGGAGTGGTCCCTTTCAT 120
Db 61 TCCAGAGGGGGCCCTGCTGCTGGGAACAACCTCAACAGAAATGGAGTGGTCCCTTTCAT 120
Qy 121 GAAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAGCTGGTGTACATTGCAGATGAA 180
Db 121 GAAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAGCTGGTGTACATTGCAGATGAA 180
Qy 181 CACCTTAATGAAGTGTCTCATATATTAGTGGTCAATGTGCTTCTTCTAGTGGCTGTAGT 240
Db 181 CACCTTAATGAAGTGTCTCATATATTAGTGGTCAATGTGCTTCTTCTAGTGGCTGTAGT 240
Qy 241 GCCTGCTGTGTGACGAGGGTCTGCACTGTGTGGGGCTAAAGACAGCAACATCACTATG 300
Db 241 GCCTGCTGTGTGACGAGGGTCTGCACTGTGTGGGGCTAAAGACAGCAACATCACTATG 300
Qy 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTACGTGGAGATGACATTCCT 360
Db 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTACGTGGAGATGACATTCCT 360
Qy 361 CAGGATGACTCTGCGAATGCGAGGCTATTCTGGAGACGACAAAGGCGAAGAGGAGAA 420
Db 361 CAGGATGACTCTGCGAATGCGAGGCTATTCTGGAGACGACAAAGGCGAAGAGGAGAA 420

Qy 421 ACCAAGGGGAGAGGAGCAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
Db 421 ACCAAGGGGAGAGGAGCAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477

RESULT 4
ADA25600
ID ADA25600 standard; cDNA; 477 BP.
XX
XX ADA25600;
XX
XX 20-NOV-2003 (first entry)
DT Rat cDNA encoding VEGF B 158 amino acid subunit.
DE
XX
XX Vulnerary; vascular endothelial cell growth;
XX vascular endothelial cell growth factor; VEGF; VEGF-A; VEGF-B; VEGF-C;
XX mitogen; vascular development; vascular repair; tissue development;
XX tissue repair; rat; ss; gene.
XX
XX Rattus sp.
XX
XX US6569434-B1.
XX
XX 27-MAY-2003.
XX
XX 30-OCT-2000; 2000US-00699769.
XX
XX 28-MAR-1991; 91US-00676436.
XX 20-SEP-1993; 93US-00124259.
XX 16-JAN-1996; 96US-00586039.
XX
XX (MERI) MERCK & CO INC.
XX
XX Bayne ML, Thomas KA;
XX WPI; 2003-605461/57.
XX P-PSDB; ADA25601.
XX
XX Stimulating vascular endothelial cell growth comprises administering an
XX amount of a vascular endothelial cell growth factor comprising a first
XX and a second C subunit amino acid sequence.
XX Example 10; Fig 8; 58pp; English.
XX The invention relates to stimulating vascular endothelial cell growth
XX comprises administering to a patient an effective vascular endothelial
XX stimulatory amount of a vascular endothelial cell growth factor (VEGF)
XX comprising a first and a second C subunit amino acid sequence, where the
XX first and second subunits comprise a sequence appearing as ADA25607. Also
XX disclosed as new are rat VEGF-A, -B and C subunit cDNAs and proteins. The
XX method and VEGF (a mitogen) are useful in inducing vascular or tissue
XX development and repair. The present sequence encodes a rat VEGF subunit.
XX
XX SQ Sequence 477 BP; 123 A; 116 C; 133 G; 105 T; 0 U; 0 Other;
Query Match 100.0%; Score 477; DB 8; Length 477;
Best Local Similarity 100.0%; Pred. No. 4.le-133;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGGCCATGAAGCTGTTCACTGCTTCTTGTGAGTCTCTAGCTGGTGGCTGTGCAC 60
Db 1 ATGCTGGCCATGAAGCTGTTCACTGCTTCTTGTGAGTCTCTAGCTGGTGGCTGTGCAC 60
Qy 61 TCCAGAGGGGGCCCTGCTGCTGGGAACAACCTCAACAGAAATGGAGTGGTCCCTTTCAT 120
Db 61 TCCAGAGGGGGCCCTGCTGCTGGGAACAACCTCAACAGAAATGGAGTGGTCCCTTTCAT 120
Qy 121 GAAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAGCTGGTGTACATTGCAGATGAA 180
Db 121 GAAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAGCTGGTGTACATTGCAGATGAA 180

QY 181 CACCCTAAGTGTCTCATATATTAGTCCGTGATGTCCTTCTGAGTCGCTGTAGT 240
 Db 181 CACCCTAAGTGTCTCATATATTAGTCCGTGATGTCCTTCTGAGTCGCTGTAGT 240
 QY 241 GGCTGTGTGTCACGAGGGTCTGCACTGTGCGCTAAAGACAGCCACATCACTATG 300
 Db 241 GGCTGTGTGTCACGAGGGTCTGCACTGTGCGCTAAAGACAGCCACATCACTATG 300
 QY 301 CAGATCTTAAAGATTCCCCCAATCGGGATCCACATTCCTACCTGGAGATGACATTTCT 360
 Db 301 CAGATCTTAAAGATTCCCCCAATCGGGATCCACATTCCTACCTGGAGATGACATTTCT 360
 QY 361 CAGGATGTACTTCGGAATCGAGCCCTATTCTGGAGACGACAAAGGAGAGAGAAA 420
 Db 361 CAGGATGTACTTCGGAATCGAGCCCTATTCTGGAGACGACAAAGGAGAGAGAAA 420
 QY 421 ACCAAGGGAAGAGGAGCAAAAGCAAAACCCACAGACTGAGGAAACCCACCTGTGA 477
 Db 421 ACCAAGGGAAGAGGAGCAAAAGCAAAACCCACAGACTGAGGAAACCCACCTGTGA 477

RESULT 5

AAQ28952
 ID AAQ28952 standard; cDNA; 477 BP.

XX AC AAQ28952;

XX DT 25-MAR-2003 (revised)

XX DT 25-FEB-1993 (first entry)

XX Sequence encoding vascular endothelial cell growth factor VEGF AB subunit B.

KW Vascular development; mitogen; blood vessel;

KW vascular endothelial growth factor; neovascularisation; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX CDS 1..477
 XX FT /*tag= a

XX EP506477-A1.

XX PD 30-SEP-1992.

XX XX 27-MAR-1992; 92EP-00302750.

XX XX 28-MAR-1991; 91US-00676436.

XX XX (MERI) MERCK & CO INC.

XX XX Bayne ML, Thomas KA;

XX DR WPI: 1992-325745/40.

XX DR P-PSDB; AAR27353.

XX Vascular endothelial cell growth factor sub-units - which stimulate
 PT vascular endothelial cell growth, used for inducing tissue repair and
 PT growth.

XX PS Example; Fig 3; 61pp; English.

XX GS-3L cells were cultured and the VEGF AB subunits were isolated and
 CC sequenced. The reduced and carboxymethylated protein eluted as two peaks
 CC at approx. 23 and 25 ml that were of approx. equal area as determined by
 CC monitored absorbance at 210 nm. Samples of the two protein subunits
 CC isolated after reduction and carboxymethylation were each applied to
 CC polybrene-coated glass fiber filters and their N-terminal sequences were
 CC determined. The peak of absorbance eluting at approx 25 ml (A subunit)
 CC yielded an amino terminal sequence Ala Pro Thr Glu Gly Glu Lys Ala
 CC His Glu Val identical to VEGF AA. The peak of absorbance eluting at
 CC approx. 23 ml (B subunit) yielded the N-terminal sequence Ala Leu Ser Ala

CC Gly Asn Xaa Ser Thr Glu Met Glu Val Val Pro Phe Asn Glu Val plus a nearly
 CC equal amount of a truncated form of the same sequence missing the first
 CC three residues. The missing X residue corresp. to an Asn in the cloned
 CC sequence. The A and sum of the B chain peptides were recovered in nearly
 CC equal amounts supporting the interpretation that the two peptides
 CC combine to form an AB heterodimer in VEGF II. The form of VEGF AB mature
 CC AB subunit in the heterodimer is the 164 amino acid form. The form of VEGF
 CC AB mature B subunit in the heterodimer is the 135 amino acid form derived
 CC from the 158 full length amino acid form. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)

XX SQ Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;

Query Match 99.7%; Score 475.4; DB 2; Length 477;

Best Local Similarity 99.8%; Pred. No. 1.2e-132;

Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGGCCATGAAGCTGTTCACTTCTTTCAGGTCCTAGCTGGTGGTGGCTGTACAC 60

Db 1 ATGCTGGCCATGAAGCTGTTCACTTCTTTCAGGTCCTAGCTGGTGGTGGCTGTACAC 60

QY 61 TCCCAGGGGGCCCTGCTGCTGGGACAACTCAACAGAAATGGAAGTGGTGGCTTTCAAT 120

Db 61 TCCCAGGGGGCCCTGCTGCTGGGACAACTCAACAGAAATGGAAGTGGTGGCTTTCAAT 120

QY 121 GAAAGTGTGGGGCCGCGAGCTACTGCCGGCCAATGGAGAAGCTGGTGTACATTGCAGATGAA 180

Db 121 GAAAGTGTGGGGCCGCGAGCTACTGCCGGCCAATGGAGAAGCTGGTGTACATTGCAGATGAA 180

QY 181 CACCCTTAATGAAGTGTCTCATATATTCAATTCAGTCGCTCATGTGCTTCTGAGTCGCTGTAGT 240

Db 181 CACCCTTAATGAAGTGTCTCATATATTCAATTCAGTCGCTCATGTGCTTCTGAGTCGCTGTAGT 240

QY 241 GCCTGTGTGGTGACGAGGGTCTGCACTGTGGCGCTAAAGACAGCCACATCACTATG 300

Db 241 GCCTGTGTGGTGACGAGGGTCTGCACTGTGGCGCTAAAGACAGCCACATCACTATG 300

QY 301 CAGATCTTAAAGATTCCCCCAATCGGGATCCACATTCCTAGCTGGAGATGACATTTCTCT 360

Db 301 CAGATCTTAAAGATTCCCCCAATCGGGATCCACATTCCTAGCTGGAGATGACATTTCTCT 360

QY 361 CAGGATGTACTCTGCGAATGCGAGGCTATTCTGGAGACGACAAAGGAGAGAGAGAAA 420

Db 361 CAGGATGTACTCTGCGAATGCGAGGCTATTCTGGAGACGACAAAGGAGAGAGAGAAA 420

QY 421 ACCAAGGGGAAGAGGAGCAAAAGCAAAACCCACAGACTGAGGAAACCCACCTGTGA 477

Db 421 ACCAAGGGGAAGAGGAGCAAAAGCAAAACCCACAGACTGAGGAAACCCACCTGTGA 477

RESULT 6

AAQ23040

ID AAQ23040 standard; DNA; 477 BP.

XX AC AAQ23040;

XX DT 29-JUL-1992 (first entry)

XX DE Encodes VEGF-II 135 amino acid B-subunit.

KW VEGF-II; mammalian glioma cell; conditioned medium; heterodimer;
 KW homodimer; mitogenesis; vascular repair; blood vessel implant;
 KW alternative splicing; ss.

XX OS Rattus.

XX FH Key Location/Qualifiers

XX sig_peptide 1..69

XX /*tag= a

XX mat_peptide 70..474

XX /*tag= b

XX /product= "VEGF-IIB"

PN EP476983-A.
 XX 25-MAR-1992.
 PD 18-SEP-1991; 91EP-00308489.
 XX 21-SEP-1990; 90US-00586638.
 PR 21-SEP-1990; 90US-00586640.
 XX (MERI) MERCK & CO INC.
 PA Bayne ML, Conn GL, Thomas KA;
 XX WPI; 1992-098641/13.
 DR P-PSDB; AAR22349.
 XX Vascular endothelial cell growth factor II - used as coating for
 PT artificial blood vessels or to promote tissue repair.
 PS Claim 22; Fig 6; 38pp; English.
 XX The B-subunit of VEGF-II occurs in two forms; the mature protein has
 CC either 135 or 115 amino acids. The two forms are generated by alternative
 CC splicing of the mRNA transcript prior to translation. The full-length
 CC coding region of the B monomer was determined from four sets of
 CC overlapping cDNA clones. PCR primers were designed based on the amino
 CC acid sequence of a Leu C peptide (L50) and used to amplify the central
 CC region of the cDNA. A single band migrating at 108bp was gel purified,
 CC digested with SalI, ligated into pGEM3zf(+) and sequenced. The nucleotide
 CC sequence obtained was used to design antisense and sense PCR primers to
 CC amplify the 5' and 3' ends of the cDNA and complete the full-length
 CC sequence. See also AAQ23038 and AAQ23041-Q23059
 XX
 SQ Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;
 Query Match 99.7%; Score 475.4; DB 2; Length 477;
 Best Local Similarity 99.8%; Pred. No. 1.2e-132;
 Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGTCCTAGCTGGTGGCTGTGCAC 60
 Db 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGTCCTAGCTGGTGGCTGTACAC 60
 QY 61 TCCAGAGGGGCGCTCTGCTGGGAACTCAACAGAAATGGAGTGGTCCCTTTCAAT 120
 Db 61 TCCAGAGGGGCGCTCTGCTGGGAACTCAACAGAAATGGAGTGGTCCCTTTCAAT 120
 QY 121 GAAAGTGTGGGGCCGAGCTACTGCGGCAATGGAGAACTGGTGTATCATTGCAGATGAA 180
 Db 121 GAAAGTGTGGGGCCGAGCTACTGCGGCAATGGAGAACTGGTGTATCATTGCAGATGAA 180
 QY 181 CACCCCTAATGAAGTGTCTCATATATTCAGTCCGTATGCTCTTCTGAGTGGCTGTAGT 240
 Db 181 CACCCCTAATGAAGTGTCTCATATATTCAGTCCGTATGCTCTTCTGAGTGGCTGTAGT 240
 QY 241 GGCTGCTGTGGTGAAGGGTCTGCACATGTTGGGCTTAAGACAGCCAACTACTATG 300
 Db 241 GGCTGCTGTGGTGAAGGGTCTGCACATGTTGGGCTTAAGACAGCCAACTACTATG 300
 QY 301 CAGATCTTAAAGATTCCCGCCCAATCGGATCCACATTCCTACGTGGAGATGACATTTCT 360
 Db 301 CAGATCTTAAAGATTCCCGCCCAATCGGATCCACATTCCTACGTGGAGATGACATTTCT 360
 QY 361 CAGGATGTACTCTGCGAATGCAAGGCTATTCTGGAGACGCAAAAGGAGAGGAAA 420
 Db 361 CAGGATGTACTCTGCGAATGCAAGGCTATTCTGGAGACGCAAAAGGAGAGGAAA 420
 QY 421 ACCAAGGGGAAGAGGAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 477
 Db 421 ACCAAGGGGAAGAGGAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 477

RESULT 7

AAV25538
 ID AAV25538 standard; cDNA; 477 BP.
 XX
 AC AAV25538;
 XX
 DT 30-JUL-1998 (first entry)
 XX Vascular endothelial growth factor II B subunit 1 encoding cDNA.
 DE Vascular endothelial cell growth factor; VEGF II; rat; glioma cell;
 XX mitogenesis; blood vessel growth; artificial blood vessel; ss.
 KW
 XX Rattus sp.
 OS
 XX Key Location/Qualifiers
 FH 1. .477
 FT CDS /tag= a
 FT /product= "VEGF II B subunit"
 XX
 XX US5726152-A.
 XX
 XX 10-MAR-1998.
 XX 31-AUG-1994; 94US-00299185.
 XX 21-SEP-1990; 90US-00586638.
 PR 05-JAN-1993; 93US-00000834.
 XX (MERI) MERCK & CO INC.
 PA Conn GL, Thomas KA, Bayne ML;
 XX WPI; 1998-206007/18.
 DR P-PSDB; AAW53646.
 XX Vascular endothelial growth factor proteins - having specified A and B
 PT sub-units.
 XX
 XX Claim 1; Fig 6; 46pp; English.
 XX The present sequence encodes a rat vascular endothelial growth factor II
 CC (VEGF II) B subunit. The present invention describes: (1) a mammalian
 CC VEGF II protein comprising an A subunit from AAW53639, AAW53640 or
 CC AAW53641, and a B subunit from AAW53638, AAW53639 or the first 115-135
 CC amino acids of AAW53638; and (2) a mammalian VEGF comprising a
 CC heterodimer or homodimer of B subunits. The growth factor is used for
 CC promoting vascular development and repair and for promoting tissue repair
 XX
 SQ Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;
 Query Match 99.7%; Score 475.4; DB 2; Length 477;
 Best Local Similarity 99.8%; Pred. No. 1.2e-132;
 Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGTCCTAGCTGGTGGCTGTGCAC 60
 Db 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGTCCTAGCTGGTGGCTGTACAC 60
 QY 61 TCCAGAGGGGCGCTCTGCTGGGAACTCAACAGAAATGGAGTGGTCCCTTTCAAT 120
 Db 61 TCCAGAGGGGCGCTCTGCTGGGAACTCAACAGAAATGGAGTGGTCCCTTTCAAT 120
 QY 121 GAAAGTGTGGGGCCGAGCTACTGCGGCAATGGAGAACTGGTGTATCATTGCAGATGAA 180
 Db 121 GAAAGTGTGGGGCCGAGCTACTGCGGCAATGGAGAACTGGTGTATCATTGCAGATGAA 180
 QY 181 CACCCCTAATGAAGTGTCTCATATATTCAGTCCGTATGCTCTTCTGAGTGGCTGTAGT 240
 Db 181 CACCCCTAATGAAGTGTCTCATATATTCAGTCCGTATGCTCTTCTGAGTGGCTGTAGT 240
 QY 241 GGCTGCTGTGGTGAAGGGTCTGCACATGTTGGGCTTAAGACAGCCAACTACTATG 300
 Db 241 GGCTGCTGTGGTGAAGGGTCTGCACATGTTGGGCTTAAGACAGCCAACTACTATG 300

```

QY 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTACGTTGAGATGACATTCTCT 360
DB 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTACGTTGAGATGACATTCTCT 360
QY 361 CAGGATCTACTCTCGGAATCAGGCTTATCTTGAGACGACAAAGGAGAGGAGAAA 420
DB 361 CAGGATCTACTCTCGGAATCAGGCTTATCTTGAGACGACAAAGGAGAGGAGAAA 420
QY 421 ACCAAGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
DB 421 ACCAAGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477

RESULT 8
AAV25536
ID AAV25536 standard; cDNA; 477 BP.
AC AAV25536;
XX
DT 30-JUL-1998 (first entry)
XX
DE Vascular endothelial growth factor I A subunit 3 encoding cDNA.
DE
KW Vascular endothelial cell growth factor; VEGF II; rat; glioma cell;
KW mitogenesis; blood vessel growth; artificial blood vessel; ss.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT 1..477
FT /*tag= a
FT /product= "VEGF I A subunit"
XX
XX US5726152-A.
XX
XX 10-MAR-1998.
XX
XX 31-AUG-1994; 94US-00299185.
XX
XX 21-SEP-1990; 90US-00586638.
XX 05-JAN-1993; 93US-00000834.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Conn GL, Thomas KA, Bayne ML;
XX
XX WPI; 1998-206007/18.
XX P-PSDB; AAW53644.
XX
XX Vascular endothelial growth factor proteins - having specified A and B
XX sub-units.
XX
XX Example 9; Fig 4; 46pp; English.
XX
XX The present sequence encodes a rat vascular endothelial growth factor I
XX (VEGF I) A subunit. The present invention describes: (i) a mammalian VEGF
XX II protein comprising an A subunit from AAW53639, AAW53640 or AAW53641,
XX and a B subunit from AAW53638, AAW53639 or the first 115-135 amino acids
XX of AAW53638; and (2) a mammalian VEGF comprising a heterodimer or
XX homodimer of B subunits. The growth factor is used for promoting vascular
XX development and repair and for promoting tissue repair
XX
SQ Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;
Query Match 99.7%; Score 475.4; DB 2; Length 477;
Best Local Similarity 99.8%; Pred. No. 1.2e-132;
Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGGCCATGAGCTGTTACTTGTCTTGTGAGGTCCTAGCTGGGTGGCTGTGCAC 60
DB 1 ATGCTGGCCATGAGCTGTTACTTGTCTTGTGAGGTCCTAGCTGGGTGGCTGTGCAC 60

```

```

QY 61 TCCACAGGGGCCCTGTCTGCTGGGAACTCACTCAAGAAATGGAAGTGGTCCCTTTCAAT 120
DB 61 TCCACAGGGGCCCTGTCTGCTGGGAACTCACTCAAGAAATGGAAGTGGTCCCTTTCAAT 120
QY 121 GAAGTGTGGGGCCGCGAGCTACTCCGGCCCAATCGAGAAAGCTGGTGTACATTGCAGATGAA 180
DB 121 GAAGTGTGGGGCCGCGAGCTACTCCGGCCCAATCGAGAAAGCTGGTGTACATTGCAGATGAA 180
QY 181 CACCCTTAATGAAGTGTCTCATATATTACGTCCGTCTGTCTCTGTAGTCCGTGTAGT 240
DB 181 CACCCTTAATGAAGTGTCTCATATATTACGTCCGTCTGTCTCTGTAGTCCGTGTAGT 240
QY 241 GGCTGTGTGGTGAACGAGGGTCTGCACTGTGTGGCGCTAAAGACAGACCAACATCACTATG 300
DB 241 GGCTGTGTGGTGAACGAGGGTCTGCACTGTGTGGCGCTAAAGACAGACCAACATCACTATG 300
QY 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTACGTTGAGATGACATTCTCT 360
DB 301 CAGATCTTAAAGATTCCCGCAATCGGATCCACATTCCTACGTTGAGATGACATTCTCT 360
QY 361 CAGGATGTACTCTCGGAATGCGAGGCTTATCTTGAGACGACAAAGGAGAGGAGAAA 420
DB 361 CAGGATGTACTCTCGGAATGCGAGGCTTATCTTGAGACGACAAAGGAGAGGAGAAA 420
QY 421 ACCAAGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
DB 421 ACCAAGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477

```

RESULT 9

AAAF81273
ID AAF81273 standard; cDNA; 477 BP.

AC AAF81273;

DT 23-NOV-2001 (first entry)

XX cDNA encoding the mature 135 amino acid form of VEGF II B subunit.

DE Rat; vascular endothelial growth factor II; VEGF-II; wound healing;
KW vascular repair; neovascularisation; tissue repair; VEGF II B subunit;
KW vulnary; angiogenesis; ss.

XX Rattus sp.

XX US6180107-B1.

XX 30-JAN-2001.

XX 10-MAR-1998; 98US-00038199.

XX 21-SEP-1990; 90US-00586638.

XX 05-JAN-1993; 93US-00000834.

XX 31-AUG-1994; 94US-00299185.

XX (MERI) MERCK & CO INC.

XX Bayne ML, Conn GL, Thomas KA;

XX WPI; 2001-256064/26.

XX P-PSDB; AAF81273.

PT Stimulating angiogenesis or wound healing through vascular repair,
PT neovascularization or both, comprises administering mammalian vascular
PT endothelial growth factor II comprising two different subunits.

XX Example 9; Fig 6; 46pp; English.

CC The invention relates to a method for stimulating angiogenesis or wound
CC healing through vascular repair, neovascularisation or both. The method
CC comprises administering to a patient a pharmaceutically effective amount
CC of mammalian vascular endothelial growth factor II (VEGF-II) comprising a
CC heterodimer of subunits A and B, or a homodimer of B subunits. VEGF-II is

CC	useful for vascular development and repair, promotion of tissue repair,	
CC	and the production of artificial vessels.	
CC	the mature 135 amino acid form of VEGF II B subunit	
XX		
SSQ	Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;	
	Query Match 99.7%; Score 475.4; DB 4; Length 477;	
	Best Local Similarity 99.8%; Pred. No. 1.2e-132;	
	Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 ATGCTGGCCATGAAGCTGTTCACTTGCTTCTGCAGGTCCCTAGCTGGTGGCTGTGCAC 60	
DB	1 ATGCTGGCCATGAAGCTGTTCACTTGCTTCTGCAGGTCCCTAGCTGGTGGCTGTGCAC 60	
QY	61 TCCAGGGGCCCTGTCTGCTGGGAAACAACCTCAACAGAAATGGAAGTGGTGCCTTCAAT 120	
DB	61 TCCAGGGGCCCTGTCTGCTGGGAAACAACCTCAACAGAAATGGAAGTGGTGCCTTCAAT 120	
QY	121 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAAGCTGGTGTACATTGCAGATGAA 180	
DB	121 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAAGCTGGTGTACATTGCAGATGAA 180	
QY	181 CACCCTAATGAAGTGTCTCATATATTCAAGTCCGTCATGTGTCCTCTCGAGTCGCTGTAGT 240	
DB	181 CACCCTAATGAAGTGTCTCATATATTCAAGTCCGTCATGTGTCCTCTCGAGTGGCTGTAGT 240	
QY	241 GGCTGCTGTGGTGACAGGGTCTGCACTGTGTGGCGCTTAAAGACAGCCAAACATCACTATG 300	
DB	241 GGCTGCTGTGGTGACAGGGTCTGCACTGTGTGGCGCTTAAAGACAGCCAAACATCACTATG 300	
QY	301 CAGATCTTAAAGATTCCCCCAATCGGGATCCCATTTCTCTACGTGGAGATGACATTTCTCT 360	
DB	301 CAGATCTTAAAGATTCCCCCAATCGGGATCCCATTTCTCTACGTGGAGATGACATTTCTCT 360	
QY	361 CAGATCTACTCTGCGAATTCAGGCGCTTATTCTGAGAGCGACAAAGGCGCAAGAGGAGAA 420	
DB	361 CAGATGTACTCTGCGAATTCAGGCGCTTATTCTGAGAGCGACAAAGGCGCAAGAGGAGAA 420	
QY	421 ACCAAGGGGAGGAGAACGAAGCAAAACCCCAACAGACTGAGGAAACCCCACTGTGA 477	
DB	421 ACCAAGGGGAGGAGAACGAAGCAAAACCCCAACAGACTGAGGAAACCCCACTGTGA 477	

RESULT 10	
AAF81272	
ID	AAF81272 standard; cDNA; 477 BP.
XX	
XX	
AC	AAF81272;
XX	
XX	
DT	23-NOV-2001 (first entry)
XX	
XX	
DE	Rat VEGF I B subunit cDNA.
XX	
XX	
KW	Rat; vascular endothelial growth factor II; VEGF-II; wound healing;
KW	vascular repair; neovascularisation; tissue repair; VEGF I B subunit;
KW	vulneraray; angiogenesis; ss.
KW	

XX	Rattus sp.	
XX	OS	
XX	PN	US6180107-B1.
XX	PN	
XX	XX	
PD	30-JAN-2001.	
XX	XX	
XX	10-MAR-1998;	98US-00038199.
XX	PF	
XX	XX	
PR	21-SEP-1990;	90US-00586638.
PR	05-JAN-1993;	93US-00000834.
PR	31-AUG-1994;	94US-00239185.
XX	XX	
PA	(MERI) MERCK & CO INC.	
XX	XX	
PI	Bayne ML, Conn GL, Thomas KA;	
XX	XX	

DR WPI; 2001-256064/26.
 DR P-PSDB; AAB/3963.
 XX
 XX Stimulating angiogenesis or wound healing through vascular repair,
 PT neovascularization or both, comprises administering mammalian vascular
 PT endothelial growth factor II comprising two different subunits.
 XX
 XX Disclosure; Fig 4I-4K; 46pp; English.
 PS
 XX The invention relates to a method for stimulating angiogenesis or wound
 XX healing through vascular repair, neovascularisation or both. The method
 CC comprises administering to a patient a pharmaceutically effective amount
 CC of mammalian vascular endothelial growth factor II (VEGF-II) comprising a
 CC heterodimer of subunits A and B, or a homodimer of B subunits. VEGF-II is
 CC useful for vascular development and repair, promotion of tissue repair,
 CC and the production of artificial vessels. The present sequence encodes
 CC VEGF I B subunit
 XX
 XX Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;
 SQ
 Query Match 99.7%; Score 475.4; DB 4; Length 477;
 Best Local Similarity 99.8%; Pred. No. 1.2e-132;
 Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0
 QY 1 ATGCTGGCAGTGAAGCTGTTCACCTGCTCTTTCGAGTCTAGCTGGTGGCGTGCAC 60
 DB 1 ATGCTGGCCATGAAGCTGTTCACCTGCTCTTTCGAGTCTAGCTGGTGGCGTGCAC 60
 QY 61 TCCACAGGGGCCCTGCTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTTCAT 120
 DB 61 TCCACAGGGGCCCTGCTCTGCTGGGAACAACCTCAACAGAAATGGAAGTGGTCCCTTTCAT 120
 QY 121 GAAGTGTGGGGCCGCGAGCTACTGCCGCCAATGGAGAAGCTGGTGTACATTCGAGATGAA 180
 DB 121 GAAGTGTGGGGCCGCGAGCTACTGCCGCCAATGGAGAAGCTGGTGTACATTCGAGATGAA 180
 QY 181 CACCCTAATGAAGTGTCTCATATATTCAGTCCGTCATGTGTCTCTGAGTCGCTGTAGT 240
 DB 181 CACCCTAATGAAGTGTCTCATATATTCAGTCCGTCATGTGTCTCTGAGTCGCTGTAGT 240
 QY 241 GGCTGCTGTGGTGAAGAGGGTCTGCATCTGTGGCGCTAAAGACAGCCAACTACTATG 300
 DB 241 GGCTGCTGTGGTGAAGAGGGTCTGCATCTGTGGCGCTAAAGACAGCCAACTACTATG 300
 QY 301 CAGATCTTAAAGATTCGCCCCCAATCGGGATCCACATTCCTACGTGGAGATGACATTCCT 360
 DB 301 CAGATCTTAAAGATTCGCCCCCAATCGGGATCCACATTCCTACGTGGAGATGACATTCCT 360
 QY 361 CAGATGTACTCTCGAATCAGGCCCTATTCTTGAGACGACAAGGCGAAGAGGAGAA 420
 DB 361 CAGATGTACTCTCGAATCAGGCCCTATTCTTGAGACGACAAGGCGAAGAGGAGAA 420
 QY 421 ACCAAGGGGAGAGGAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
 DB 421 ACCAAGGGGAGAGGAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
 RESULT 11
 ACA62374
 ID ACA62374 standard; cDNA; 477 BP.
 XX
 XX ACA62374;
 XX
 XX 19-AUG-2003 (first entry)
 DT
 XX cDNA encoding rat VEGF II B subunit.
 DE
 XX Rat; vascular endothelial growth factor II; VEGF II; mitogenesis;
 KW mammalian; vascular endothelial cell growth; tissue repair;
 KW vascular development; vascular repair; blood vessel growth;
 KW neovascularisation; artificial blood vessel; polymeric vessel; vulnerable;
 XX B subunit; gene; ss.
 XX

RESULT 11
ACA62374
ID ACA62374 standard; cDNA; 477 BP.
XX
XX ACA62374;
AC
XX
XX 19-AUG-2003 (first entry)
DT
XX
XX cDNA encoding rat VEGF II B subunit.
DE
XX
XX Rat; vascular endothelial growth factor II; VEGF II; mitogenesis;
KW mammalian; vascular endothelial cell growth; tissue repair;
KW vascular development; vascular repair; blood vessel growth;
KW neovascularisation; artificial blood vessel; polymeric vessel; vulneryary;
B subunit; gene; ss.
KW
XX

```

OS Rattus sp.
XX Key Location/Qualifiers
XX CDS 1..477
XX FT /*tag= a
XX FT /product= "VEGF II B subunit"
XX PN US2003045471-A1.
XX XX
XX PD 06-MAR-2003.
XX PF
XX PF 08-FEB-2002; 2002US-00071370.
XX PR 21-SEP-1990; 90US-00586638.
XX PR 05-JAN-1993; 93US-00000834.
XX PR 31-AUG-1994; 94US-00299185.
XX PR 10-MAR-1998; 98US-00038199.
XX PR 07-JUN-1999; 99US-00326879.
XX PA (MERI ) MERCK & CO INC.
XX PI Bayne ML, Conn GL, Thomas KA;
XX XX
XX DR WPI; 2003-371473/35.
XX DR P-PSDB; ABU62005.
XX XX
XX PT New heterodimeric vascular endothelial growth factor II comprising A and
XX PT B subunits encoded by different genes, useful for preparing a composition
XX PT for promoting vascular or tissue repair or neovascularization.
XX PS Claim 6; Fig 6; 50pp; English.
XX XX
XX CC The present invention relates to the isolation of vascular endothelial
XX CC growth factor II (VEGF II), and the polynucleotide sequences encoding it.
XX CC VEGF II is a heterodimer comprising A and B subunits that are encoded by
XX CC different genes. VEGF II stimulates mitogenesis of mammalian vascular
XX CC endothelial cells. VEGF II is useful for promoting tissue repair and for
XX CC stimulating the growth of vascular endothelial cells. VEGF II can also be
XX CC used for stimulating the growth of vascular endothelial cells in a
XX CC patient to promote vascular development and repair, or blood vessel
XX CC growth (neovascularisation). VEGF II can further be used to produce
XX CC artificial blood vessels by treating synthetic polymeric vessels with
XX CC VEGF II and implanting into them into a patient. After the implantation
XX CC endothelial cells migrate into and grow on the artificial surface. The
XX CC present sequence encodes rat VEGF II B subunit
XX SQ Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;

Query Match 99.7%; Score 475.4; DB 7; Length 477;
Best Local Similarity 99.8%; Pred. No. 1.2e-132;
Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGCCATGAAGCTGTTCACCTTCTTGCGAGTCTAGCTGGTGGCTGTGCAC 60
DB 1 ATGCTGCCATGAAGCTGTTCACCTTCTTGCGAGTCTAGCTGGTGGCTGTGCAC 60
QY 61 TCCAGGGGCCCTGTCTCTGGGAACAACCTCAACAGAATGAAGTGTGCTTTCAAT 120
DB 61 TCCAGGGGCCCTGTCTCTGGGAACAACCTCAACAGAATGAAGTGTGCTTTCAAT 120
QY 121 GAAGTGTGGGGCGGAGCTACTGCGGCCAATGGAGAGCTGGTGTACATTCAGATGA 180
DB 121 GAAGTGTGGGGCGGAGCTACTGCGGCCAATGGAGAGCTGGTGTACATTCAGATGA 180
QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTGTCATGTCCTTCTAGTGGCTGTAGT 240
DB 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTGTCATGTCCTTCTAGTGGCTGTAGT 240
QY 241 GCTGCTGTGTGACAGAGGTGTGCACTGTGTGGGCTTAAGACAGCCCAACATCAATATG 300
DB 241 GCTGCTGTGTGACAGAGGTGTGCACTGTGTGGGCTTAAGACAGCCCAACATCAATATG 300
QY 301 CAGATCTTAAAGATTCCCGCCCAATCGGGATCCACATTCCTACGTGGAGATGACATTCCT 360

```

```

DB 301 CAGATCTTAAAGATTCCCGCCCAATCGGGATCCACATTCCTACGTGGAGATGACATTCCT 360
QY 361 CAGGATGTACTCTGCGAATCGAGCCCTATTCTCGAGACGACAAAGGCGAAGAGGAGAA 420
DB 361 CAGGATGTACTCTGCGAATCGAGCCCTATTCTCGAGACGACAAAGGCGAAGAGGAGAA 420
QY 421 ACCAAGGGGAGAGGAGGAGCAAAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
DB 421 ACCAAGGGGAGAGGAGGAGCAAAAGCAAAACCCACAGACTGAGGAACCCACCTGTGA 477

RESULT 12
ACA62371
ID ACA62371 standard; cDNA; 477 BP.
XX AC ACA62371;
XX DT 19-AUG-2003 (first entry)
XX XX
XX cDNA encoding rat VEGF I A subunit cleavage product #2.
XX DE
XX KW Rat; vascular endothelial growth factor II; VEGF II; mitogenesis;
XX KW mammalian; vascular endothelial cell growth; tissue repair;
XX KW vascular development; vascular repair; blood vessel growth;
XX KW neovascularisation; artificial blood vessel; polymeric vessel; vulnery;
XX KW A subunit; gene; ss.
XX OS Rattus sp.
XX XX
XX Key Location/Qualifiers
XX CDS 1..477
XX FT /*tag= a
XX FT /product= "VEGF I A subunit cleavage product #2"
XX PN US2003045471-A1.
XX XX
XX PD 06-MAR-2003.
XX PF
XX PF 08-FEB-2002; 2002US-00071370.
XX PR 21-SEP-1990; 90US-00586638.
XX PR 05-JAN-1993; 93US-00000834.
XX PR 31-AUG-1994; 94US-00299185.
XX PR 10-MAR-1998; 98US-00038199.
XX PR 07-JUN-1999; 99US-00326879.
XX PA (MERI ) MERCK & CO INC.
XX PI Bayne ML, Conn GL, Thomas KA;
XX XX
XX DR WPI; 2003-371473/35.
XX DR P-PSDB; ABU62003.
XX XX
XX PT New heterodimeric vascular endothelial growth factor II comprising A and
XX PT B subunits encoded by different genes, useful for preparing a composition
XX PT for promoting vascular or tissue repair or neovascularization.
XX PS Example 9; Fig 41-4K; 50pp; English.
XX XX
XX CC The present invention relates to the isolation of vascular endothelial
XX CC growth factor II (VEGF II), and the polynucleotide sequences encoding it.
XX CC VEGF II is a heterodimer comprising A and B subunits that are encoded by
XX CC different genes. VEGF II stimulates mitogenesis of mammalian vascular
XX CC endothelial cells. VEGF II is useful for promoting tissue repair and for
XX CC stimulating the growth of vascular endothelial cells. VEGF II can also be
XX CC used for stimulating the growth of vascular endothelial cells in a
XX CC patient to promote vascular development and repair, or blood vessel
XX CC growth (neovascularisation). VEGF II can further be used to produce
XX CC artificial blood vessels by treating synthetic polymeric vessels with
XX CC VEGF II and implanting into them into a patient. After the implantation
XX CC endothelial cells migrate into and grow on the artificial surface. The
XX CC present sequence encodes rat VEGF I A subunit cleavage product #2

```


XX SQ Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;

Query Match 99.7%; Score 475.4; DB 7; Length 477;
 Best Local Similarity 99.8%; Pred. No. 1.2e-132;
 Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGCCATGAAGCTGTTCACCTTGCTTCTTGCAGTCTCTAGTGGTGGCTGTGCAC 60
 DB 1 ATGCTGCCATGAAGCTGTTCACCTTGCTTCTTGCAGTCTCTAGTGGTGGCTGTGCAC 60

QY 61 TCCAGGGGCGCTGTCTGTCTGGGAAACAACCTCAACAGAAATGGAAGTGGCTTCAAT 120
 DB 61 TCCAGGGGCGCTGTCTGTCTGGGAAACAACCTCAACAGAAATGGAAGTGGCTTCAAT 120

QY 121 GAAGTGTGGGGCGCAGCTACTGCGGCCCAATGAGAGAGCTGGTGTACATTGCAGATGAA 180
 DB 121 GAAGTGTGGGGCGCAGCTACTGCGGCCCAATGAGAGAGCTGGTGTACATTGCAGATGAA 180

QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCATGTGTCTTCTGAGTGGCTGTAGT 240
 DB 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCATGTGTCTTCTGAGTGGCTGTAGT 240

QY 241 GGCTGTGTGTGACAGAGGTCTGCATCTGTGTGGCGCTAAAGACAGCAACATCACTATG 300
 DB 241 GGCTGTGTGTGACAGAGGTCTGCATCTGTGTGGCGCTAAAGACAGCAACATCACTATG 300

QY 301 CAGATCTTAAGATTCCTCGAATCGAGGATCCACATTCCTACGTGGAGATGACATTTCT 360
 DB 301 CAGATCTTAAGATTCCTCGAATCGAGGATCCACATTCCTACGTGGAGATGACATTTCT 360

QY 361 CAGATGTACTCTCGAATCGAGGATCCACATTCCTACGTGGAGATGACATTTCT 420
 DB 361 CAGATGTACTCTCGAATCGAGGATCCACATTCCTACGTGGAGATGACATTTCT 420

QY 421 ACCAAGGGGAGAGCAAGCAAAAGCAAAACCCACAGACTGAGAACCCACCTGTGA 477
 DB 421 ACCAAGGGGAGAGCAAGCAAAAGCAAAACCCACAGACTGAGAACCCACCTGTGA 477

RESULT 13
 AAQ28955
 ID AAQ28955 standard; cDNA; 417 BP.

XX AC AAQ28955;
 XX AC AAQ28955;
 DT 25-MAR-2003 (revised)
 DT 25-FEB-1993 (first entry)

XX DE Sequence encoding vascular endothelial cell growth factor VEGF B 138
 XX DE amino acid residue subunit.

XX KW Vascular development; mitogen; blood vessel;
 XX KW vascular endothelial growth factor; neovascularisation; ss.

XX OS Rattus.

XX FH Key Location/Qualifiers
 FT CDS 1..417
 FT /*tag= a

XX PN EP506477-A1.
 XX PD 30-SEP-1992.

XX PF 27-MAR-1992; 92EP-00302750.
 XX PR 28-MAR-1991; 91US-00676436.
 XX PA (MERI) MERCK & CO INC.
 XX PI Bayne ML, Thomas KA;
 XX PH Location/Qualifiers

DR WPI; 1992-325745/40.
 XX P-PSDB; AAR27356.

PT Vascular endothelial cell growth factor sub-units - which stimulate
 PT vascular endothelial cell growth, used for inducing tissue repair and
 PT growth.

XX PS Disclosure; Fig 7; 61pp; English.

XX CC The full length coding region of the B subunit or monomer of VEGF is
 CC determined from four sets of overlapping cDNA clones. Degenerate oligo-
 CC primers based on the amino acid sequences from polypeptide L50 are used
 CC to PCR amplify the central region of the cDNA for VEGF AB, B monomer. A
 CC single band migrating at 108 bp was gel purified, digested with SalI,
 CC ligated into pGEM3zf(+) and sequenced. The nucleotide sequence obtained
 CC (pYG) was used to design antisense and sense PCR primers to amplify the
 CC 5' and 3' ends of the cDNA. These 5' and 3' clones are denoted p5V2 and
 CC p3V2 respectively. The entire base sequence for the 158 amino acid
 CC microheterogeneous B subunit and the 138 amino acid microheterogeneous B
 CC subunit are shown in AAQ28955 and AAQ28956. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)

XX SQ Sequence 417 BP; 98 A; 100 C; 116 G; 103 T; 0 U; 0 Other;

Query Match 86.8%; Score 414; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3.4e-114;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCCATGAAGCTGTTCACCTTGCTTCTTGCAGTCTCTAGTGGTGGCTGTGCAC 60
 DB 1 ATGCTGCCATGAAGCTGTTCACCTTGCTTCTTGCAGTCTCTAGTGGTGGCTGTGCAC 60

QY 61 TCCAGGGGCGCTGTCTGTCTGGGAAACAACCTCAACAGAAATGGAAGTGGCTTCAAT 120
 DB 61 TCCAGGGGCGCTGTCTGTCTGGGAAACAACCTCAACAGAAATGGAAGTGGCTTCAAT 120

QY 121 GAAGTGTGGGGCGCAGCTACTGCGGCCCAATGAGAGAGCTGGTGTACATTGCAGATGAA 180
 DB 121 GAAGTGTGGGGCGCAGCTACTGCGGCCCAATGAGAGAGCTGGTGTACATTGCAGATGAA 180

QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCATGTGTCTTCTGAGTGGCTGTAGT 240
 DB 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCATGTGTCTTCTGAGTGGCTGTAGT 240

QY 241 GGCTGTGTGTGACAGAGGTCTGCATCTGTGTGGCGCTAAAGACAGCAACATCACTATG 300
 DB 241 GGCTGTGTGTGACAGAGGTCTGCATCTGTGTGGCGCTAAAGACAGCAACATCACTATG 300

QY 301 CAGATCTTAAGATTCCTCGAATCGAGGATCCACATTCCTACGTGGAGATGACATTTCT 360
 DB 301 CAGATCTTAAGATTCCTCGAATCGAGGATCCACATTCCTACGTGGAGATGACATTTCT 360

QY 361 CAGATGTACTCTCGAATCGAGGATCCACATTCCTACGTGGAGATGACATTTCT 414
 DB 361 CAGATGTACTCTCGAATCGAGGATCCACATTCCTACGTGGAGATGACATTTCT 414

RESULT 14
 AAQ39829
 ID AAQ39829 standard; cDNA; 417 BP.

XX AC AAQ39829;
 XX AC AAQ39829;
 DT 15-FEB-2000 (first entry)

XX DE VEGFB 138 amino acid residue subunit nucleotide sequence.

XX DE VEGF; vascular endothelial growth factor; B subunit; tissue growth;
 XX KW vascular development; artificial blood vessel; repair; human; ss.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers

```

FT CDS      1. .417
FT          /*tag= a
FT          /product= "VEGFB"
FT          /note= "138 amino acid subunit"
XX
XX US5994300-A.
XX
XX 30-NOV-1999.
XX
XX 20-SEP-1993; 93US-00124259.
XX
XX 28-MAR-1991; 91US-00676436.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Thomas KA, Bayne ML;
XX
XX WPI; 2000-038268/03.
XX
XX P-PSDB; AAY57031.
XX
XX Purified and isolated vascular endothelial cell growth factor C subunit
XX for the induction of tissue repair or growth.
XX
XX Disclosure; Fig 7; 58pp; English.
XX
XX This is the nucleotide sequence of a 138 amino acid residue B subunit of
XX vascular endothelial cell growth factor (VEGF). The invention relates to
XX a purified and isolated VEGF C subunit amino acid sequence AAY57025. VEGF
XX exists in various microheterogeneous forms, and is useful for the
XX promotion of vascular development and repair. The invention also relates
XX to human VEGF heterodimers AC or BC and homodimer CC, where A, B and C
XX are subunit amino acid sequences. The VEGF AC, BC or CC amino acid
XX sequences can be used in a tissue repairing pharmaceutical composition.
XX The novel growth factors are useful for the production or coverage of
XX artificial blood vessels with vascular endothelial cell. They are also
XX useful for the induction of tissue growth and repair
XX
XX Sequence 417 BP; 98 A; 100 C; 116 G; 103 T; 0 U; 0 Other;
XX
XX Query Match      86.8%; Score 414; DB 3; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-114;
XX Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ATGCTGGCCATGAAGCTGTCTCTCTGCGGAACTCAACAGAAATGGAAGTGGCTTTCAAT 120
XX |
XX DB 1 ATGCTGGCCATGAAGCTGTCTCTCTGCGGAACTCAACAGAAATGGAAGTGGCTTTCAAT 120
XX |
XX QY 61 TCCAGGGGGCCCTGTCTCTGCGGAACTCAACAGAAATGGAAGTGGCTTTCAAT 120
XX |
XX DB 61 TCCAGGGGGCCCTGTCTCTGCGGAACTCAACAGAAATGGAAGTGGCTTTCAAT 120
XX |
XX QY 121 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAACTGGTGATTCAGATGAA 180
XX |
XX DB 121 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAACTGGTGATTCAGATGAA 180
XX |
XX QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTATGTCTCTGAGTGGCTGTAGT 240
XX |
XX DB 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTATGTCTCTGAGTGGCTGTAGT 240
XX |
XX QY 241 GCCTCTGTGTGACGAGGGTCTGCATATATTCAGTCCGTATGTCTCTGAGTGGCTGTAGT 300
XX |
XX DB 241 GCCTCTGTGTGACGAGGGTCTGCATATATTCAGTCCGTATGTCTCTGAGTGGCTGTAGT 300
XX |
XX QY 301 CAGATCTTAAAGATTCCCGCCCAATCGGGATCCACATTCCTAGTGGAGATGACATTCCT 360
XX |
XX DB 301 CAGATCTTAAAGATTCCCGCCCAATCGGGATCCACATTCCTAGTGGAGATGACATTCCT 360
XX |
XX QY 361 CAGGATGTACTCTCGAATGACAGGCTATTTCTGGAGACACAAAGCAGAAAGG 414
XX |
XX DB 361 CAGGATGTACTCTCGAATGACAGGCTATTTCTGGAGACACAAAGCAGAAAGG 414
XX
XX RESULT 15

```

```

AAC83514
ID AAC83514 standard; cDNA; 417 BP.
XX
XX AAC83514;
AC
XX
XX 26-FEB-2001 (first entry)
DT
XX
XX Rat VEGF subunit B coding sequence SEQ ID NO: 36.
DE
XX
XX Vascular endothelial growth factor; VEGF C subunit; cell division;
XX artificial blood vessel; tissue growth; tissue repair; ss.
XX
XX Rattus sp.
XX
XX US6140073-A.
XX
XX 31-OCT-2000.
XX
XX 16-JAN-1996; 96US-00586039.
XX
XX 28-MAR-1991; 91US-00676436.
XX
XX 20-SEP-1993; 93US-00124259.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Thomas KA, Bayne ML;
XX
XX WPI; 2001-014858/02.
XX
XX P-PSDB; AAB37507.
XX
XX Human vascular endothelial cell growth factor (VEGF) C subunit DNA and
XX protein, useful for promoting vascular development and repair, and for
XX promoting tissue repair, especially for treating wounds in mammals.
XX
XX Example 10; Fig 7; 58pp; English.
XX
XX The present invention is concerned with the human vascular endothelial
XX growth factor (VEGF) C subunit. VEGF is a vascular endothelial cell
XX mitogen and can be used to promote vascular development and repair. The C
XX subunit may exist as a homodimer or a heterodimer with the VEGF A or B
XX subunit. VEGF can be used in the treatment of wounds of mammals, to cover
XX artificial blood vessels with vascular endothelial cells, in the
XX production of artificial blood vessels and to induce tissue repair or
XX growth
XX
XX Sequence 417 BP; 98 A; 100 C; 116 G; 103 T; 0 U; 0 Other;
XX
XX Query Match      86.8%; Score 414; DB 4; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-114;
XX Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ATGCTGGCCATGAAGCTGTCTCTCTGCGGAACTCAACAGAAATGGAAGTGGCTTTCAAT 120
XX |
XX DB 1 ATGCTGGCCATGAAGCTGTCTCTCTGCGGAACTCAACAGAAATGGAAGTGGCTTTCAAT 120
XX |
XX QY 61 TCCAGGGGGCCCTGTCTCTGCGGAACTCAACAGAAATGGAAGTGGCTTTCAAT 120
XX |
XX DB 61 TCCAGGGGGCCCTGTCTCTGCGGAACTCAACAGAAATGGAAGTGGCTTTCAAT 120
XX |
XX QY 121 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAACTGGTGATTCAGATGAA 180
XX |
XX DB 121 GAAGTGTGGGGCCGAGCTACTGCGGCCAATGGAGAACTGGTGATTCAGATGAA 180
XX |
XX QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTATGTCTCTGAGTGGCTGTAGT 240
XX |
XX DB 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTATGTCTCTGAGTGGCTGTAGT 240
XX |
XX QY 241 GCCTCTGTGTGACGAGGGTCTGCATATATTCAGTCCGTATGTCTCTGAGTGGCTGTAGT 300
XX |
XX DB 241 GCCTCTGTGTGACGAGGGTCTGCATATATTCAGTCCGTATGTCTCTGAGTGGCTGTAGT 300
XX |
XX QY 301 CAGATCTTAAAGATTCCCGCCCAATCGGGATCCACATTCCTAGTGGAGATGACATTCCT 360
XX |

```

Db 301 CAGATCTTAAAGATTCCCCCAATCGGATCCACATTCTACGTGAGATGACATTCTCT 360
Qy 361 CAGGATGTAATGCGAATGCGGCTATTCTGGAGACGACAAAGGCAGAAAGG 414
Db 361 CAGGATGTAATGCGAATGCGGCTATTCTGGAGACGACAAAGGCAGAAAGG 414

Search completed: September 16, 2004, 20:53:23
Job time : 309 secs

Blank Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 20:53:28 ; Search time 348 Seconds
(without alignments)

6918.483 Million cell updates/sec

Title: US-10-071-370A-3

Perfect score: 477

Sequence: 1 atgtgtgcatgaagtgtt.....ctgaggaaccccaactgtga 477

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	477	15	US-10-071-370A-3
2	414	86.8	417	15	US-10-071-370A-5
3	213.6	44.8	1645	9	US-09-795-006A-114
4	213.6	44.8	1645	13	US-10-211-462-114
5	213.6	44.8	1645	15	US-10-262-538-27
6	213.6	44.8	1645	15	US-10-007-926A-103
7	213.6	44.8	1645	15	US-10-101-510-590
8	213.6	44.8	1645	15	US-10-021-660-35
9	213.2	44.7	468	13	US-10-343-825A-11
10	187.6	39.3	450	13	US-10-343-825A-12
11	168.4	35.3	475	10	US-09-918-995-1813
12	147.4	30.9	474	13	US-10-343-825A-13
13	121.8	25.5	474	13	US-10-343-825A-14
14	109	22.9	1104	10	US-09-832-355A-93

15	108.8	22.8	670	16	US-10-294-228-5	Sequence 5, Appli
16	108.8	22.8	677	15	US-10-189-360-3	Sequence 3, Appli
17	108.8	22.8	728	15	US-10-189-360-4	Sequence 4, Appli
18	108.4	22.7	576	15	US-10-419-045-3	Sequence 3, Appli
19	107.6	22.6	645	12	US-10-152-319A-1958	Sequence 1958, Ap
20	107.6	22.6	645	17	US-10-664-705-3	Sequence 3, Appli
21	107.2	22.5	516	9	US-09-812-133-1	Sequence 1, Appli
22	107.2	22.5	516	14	US-10-083-817-7	Sequence 7, Appli
23	107.2	22.5	516	15	US-10-268-447-3	Sequence 3, Appli
24	107.2	22.5	516	15	US-10-319-828-1	Sequence 1, Appli
25	107.2	22.5	516	15	US-10-392-331-3	Sequence 3, Appli
26	107.2	22.5	516	16	US-10-418-529-3	Sequence 3, Appli
27	107.2	22.5	545	15	US-10-293-157-1	Sequence 1, Appli
28	107.2	22.5	642	14	US-10-083-817-9	Sequence 9, Appli
29	107.2	22.5	642	15	US-10-268-447-7	Sequence 7, Appli
30	107.2	22.5	642	15	US-10-392-331-7	Sequence 7, Appli
31	107.2	22.5	642	16	US-10-418-529-7	Sequence 7, Appli
32	107.2	22.5	645	13	US-10-370-291-5	Sequence 5, Appli
33	107.2	22.5	648	16	US-10-294-228-4	Sequence 4, Appli
34	107.2	22.5	665	15	US-10-293-157-29	Sequence 29, Appli
35	107.2	22.5	696	13	US-10-370-291-7	Sequence 7, Appli
36	107.2	22.5	699	14	US-10-083-817-10	Sequence 10, Appli
37	107.2	22.5	699	15	US-10-268-447-9	Sequence 9, Appli
38	107.2	22.5	699	16	US-10-392-331-9	Sequence 9, Appli
39	107.2	22.5	785	16	US-10-418-529-9	Sequence 9, Appli
40	107.2	22.5	785	16	US-10-191-997-114	Sequence 114, App
41	107.2	22.5	815	9	US-09-795-006A-146	Sequence 146, App
42	105.8	22.2	1116	10	US-09-832-355A-88	Sequence 88, Appl
43	105.6	22.1	426	13	US-09-884-050-1	Sequence 1, Appli
44	105.6	22.1	426	15	US-10-298-794-1	Sequence 1, Appli
45	105.6	22.1	495	15	US-10-293-157-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-10-071-370A-3
; Sequence 3, Application US/10071370A
; Publication No. US20030045471A1
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas, Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
; TITLE OF INVENTION: II
; FILE REFERENCE: 18199CB
; CURRENT APPLICATION NUMBER: US/10/071.370A
; CURRENT FILING DATE: 2002-02-08
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: 09/326,879
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: 09/038,199
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/299,185
; PRIOR FILING DATE: 1994-08-31
; PRIOR APPLICATION NUMBER: 08/000,834
; PRIOR FILING DATE: 1993-01-05
; PRIOR APPLICATION NUMBER: 07/586,638
; PRIOR FILING DATE: 1990-09-21
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 477
; TYPE: DNA
; ORGANISM: rat
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(477)

US-10-071-370A-3
Query Match 100.0%; Score 477; DB 15; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.6e-156;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGCTCTAGCTGGTGGCTGTGCAC 60
 Db 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGCTCTAGCTGGTGGCTGTGCAC 60
 QY 61 TCCAGGGGGCCCTGTCTGTGGGAACTCAACTCAAGAAATGGAAGTGGCTTTCAAT 120
 Db 61 TCCAGGGGGCCCTGTCTGTGGGAACTCAACTCAAGAAATGGAAGTGGCTTTCAAT 120
 QY 121 GAAGTGTGGGGCCGAGCTACTCCGGCCAAATGGAAGTGGTGTACATGAGATGAA 180
 Db 121 GAAGTGTGGGGCCGAGCTACTCCGGCCAAATGGAAGTGGTGTACATGAGATGAA 180
 QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCAATGCTTCTGAGTGGCTGTAGT 240
 Db 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCAATGCTTCTGAGTGGCTGTAGT 240
 QY 241 GGCTGTGTGGTGAAGGCTGTGCACTGTGTGGCGCTAAAGACAGCAATCACTATG 300
 Db 241 GGCTGTGTGGTGAAGGCTGTGCACTGTGTGGCGCTAAAGACAGCAATCACTATG 300
 QY 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTGAGATGACATTTCTCT 360
 Db 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTGAGATGACATTTCTCT 360
 QY 361 CAGGATGTACTCTGCGAATGCGAGGCTATTCTGGAGACGACAAAGGAGGAAA 420
 Db 361 CAGGATGTACTCTGCGAATGCGAGGCTATTCTGGAGACGACAAAGGAGGAAA 420
 QY 421 ACCAAGGGGAAGAGGAGCAAGCAAAACCCACAGACTGAGGACCCACCTGTGA 477
 Db 421 ACCAAGGGGAAGAGGAGCAAGCAAAACCCACAGACTGAGGACCCACCTGTGA 477

RESULT 2

US-10-071-370A-5
 ; Sequence 5, Application US/10071370A
 ; Publication No. US20030045471A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayne, Marvin L.
 ; APPLICANT: Conn, Gregory L.
 ; APPLICANT: Thomas, Jr., Kenneth A.
 ; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
 ; FILE REFERENCE: 18199CB
 ; CURRENT APPLICATION NUMBER: US/10/071,370A
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: 09/326,879
 ; PRIOR FILING DATE: 1999-06-07
 ; PRIOR APPLICATION NUMBER: 09/038,199
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 08/299,185
 ; PRIOR FILING DATE: 1994-08-31
 ; PRIOR APPLICATION NUMBER: 08/000,834
 ; PRIOR FILING DATE: 1993-01-05
 ; PRIOR APPLICATION NUMBER: 07/586,638
 ; PRIOR FILING DATE: 1990-09-21
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 417
 ; TYPE: DNA
 ; ORGANISM: rat
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(417)
 US-10-071-370A-5
 Query Match 86.8%; Score 414; DB 15; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3e-134;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGCTCTAGCTGGTGGCTGTGCAC 60

Db 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGCTCTAGCTGGTGGCTGTGCAC 60
 QY 61 TCCAGGGGGCCCTGTCTGTGGGAACTCAACTCAAGAAATGGAAGTGGCTTTCAAT 120
 Db 61 TCCAGGGGGCCCTGTCTGTGGGAACTCAACTCAAGAAATGGAAGTGGCTTTCAAT 120
 QY 121 GAAGTGTGGGGCCGAGCTACTCCGGCCAAATGGAAGTGGTGTACATGAGATGAA 180
 Db 121 GAAGTGTGGGGCCGAGCTACTCCGGCCAAATGGAAGTGGTGTACATGAGATGAA 180
 QY 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCAATGCTTCTGAGTGGCTGTAGT 240
 Db 181 CACCTTAATGAAGTGTCTCATATATTCAGTCCGTCAATGCTTCTGAGTGGCTGTAGT 240
 QY 241 GGCTGTGTGGTGAAGGCTGTGCACTGTGTGGCGCTAAAGACAGCAATCACTATG 300
 Db 241 GGCTGTGTGGTGAAGGCTGTGCACTGTGTGGCGCTAAAGACAGCAATCACTATG 300
 QY 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTGAGATGACATTTCTCT 360
 Db 301 CAGATCTTAAAGATTCCTCCCAATCGGATCCACATTCCTGAGATGACATTTCTCT 360
 QY 361 CAGGATGTACTCTGCGAATGCGAGGCTATTCTGGAGACGACAAAGGAGGAAA 414
 Db 361 CAGGATGTACTCTGCGAATGCGAGGCTATTCTGGAGACGACAAAGGAGGAAA 414

RESULT 3

US-09-795-006A-114
 ; Sequence 114, Application US/09795006A
 ; Patent No. US20020151680A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alitalo et al
 ; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
 ; FILE REFERENCE: 28967/35977B
 ; CURRENT APPLICATION NUMBER: US/09/795,006A
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: US 60/205,331
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 60/185,205
 ; PRIOR FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 114
 ; LENGTH: 1645
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (322)...(768)
 US-09-795-006A-114
 Query Match 44.8%; Score 213.6; DB 9; Length 1645;
 Best Local Similarity 68.3%; Pred. No. 1.1e-63;
 Matches 332; Conservative 0; Mismatches 139; Indels 15; Gaps 2;
 QY 1 ATGCTGGCCATGAAGCTGTTCACTTCTTCTGAGGCTCTAGCTGGTGGCTGTGCAC 60
 Db 322 ATGCGGTCATGAGGCTGTTCCCTTCTTCTGAGCTCTCTGCGGGCTGGGCTGCT 381
 QY 61 TCC-----CAGGGGGCCCTGTCTGCTGGGAACTCACTCAAGAAATGGAAGT 108
 Db 382 GCTGTGCCCCCAGCAGTGGGCTTGTCTGCTGGGAACTGCTGTCAGAGGTGGAAGT 441
 QY 109 GTGCTTTCAATGAAGTGTGGGCGCAGCTACTCGCGGCAATGGAAGTGGTGTAC 168
 Db 442 GTACCTTCCAGGAAGTGTGGGCGCAGCTACTCGCGGCGCTGGAGAGCTGGTGCAC 501
 QY 169 ATTGCAGATGAACACCCCAATGAAGTGTCTCATATATTCAGTCCGTCATGTCTCTG 228
 Db 502 GTCGTGTCGAGTACCCAGGAGGTGGAGCAGATGTTTACGCCCATCTGTGTCTCCCTG 561

QY 409 GAAAGGAGGAAACCAAGGGAGAGGAAGCAAGCAAAACCCACAGACTGAGGAACCC 468

US-10-021-660-35
US-10-021-660-35
; Sequence 35, Application US/10021660


```

; CURRENT APPLICATION NUMBER: US/10/343,825A
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/JP01/06856
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence encoding Chimeric VEGF protein
US-10-343-825A-11

Query Match 44.7%; Score 213.2; DB 13; Length 468;
Best Local Similarity 72.4%; Pred.No. 8.2e-64;
Matches 310; Conservative 0; Mismatches 103; Indels 15; Gaps 2;

QY 1 ATGCTGCCAATGAAGCTGTTCACTTGCTCTTCTGCAGGTCCCTAGCTGGGCTGGCTGTGCAC 60
Db 1 ATGCCGCTCATGAGGCTGTTCCCTTGCTTCTGCAGCTCCTGGCCGGCTGGCGCTGCCT 60
QY 61 TCC-----CAGGGGGCCCTGCTCTGCTGGGAACAACTCAAAGAAATGGAAGTG 108
Db 61 GCTGTGCCCCCCAGCAGTGGGCTTGTCTGCTGGGAACGCTCCTCAGAGTGGAGTG 120
QY 109 GTGCCCTTCAATGAAGTGTGGGCGCAGCTACTGCGGCCCAATGGAGAACCTGGTGAC 168
Db 121 GTACCTTCCAGAAAGTGTGGGCGCAGCTACTGCGGGCGCTGGAGAGGCTGGTGAC 180
QY 169 ATTGCAGATGAACACCCCTAATGAAGTGTCTCATATATTCAGTCCGCTCATGTGCTCTG 228
Db 181 GTCGTGTCCAGTATCCCCACGAGGTGGAGCAGATGTTACGCCCATCTGTGCTCTCCCTG 240
QY 229 AGTCGCTGTAGTGGCTGCTCTGTGTGACGAGGGTCTGCACGTGTGTGGCGCTAAAGACAGCC 288
Db 241 CTGCGCTGCACCGGCTGCTCGGCGATGAGAACTGCACTGTGTGCGGTGGAGACGCGCC 300
QY 289 AACATCACTATGACAGATCTTAAGATTCGCCCAATCGGGATCCACATTCCTCTAGCTGGAG 348
Db 301 AATGTCACCATGAGCTCCTAAAGAT---CGTTCTGGGGACCGGCCCTCCTACGTGGAG 357
QY 349 ATGCATTTCTCAGGATGTACTCTGCGAATGCAAGGCTATTTCTGGAGACGACAAAGCA 408
Db 358 CTGAGCTTCTCAGACAGTTCGCTGGAATGCCGGCTCTGCGGGAAGATGAAGCGG 417
QY 409 GAAAGGAG 416
Db 418 GAAAGGTG 425

RESULT 10
US-10-343-825A-12
; Sequence 12, Application US/10343825A
; Publication No. US20040038341A1
; GENERAL INFORMATION:
; APPLICANT: SHIBUYA, Masabumi
; TITLE OF INVENTION: Chimeric Human-Type Vascular Endothelial Cell Growth Fac
; FILE REFERENCE: P23303
; CURRENT APPLICATION NUMBER: US/10/343,825A
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/JP01/06856
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence encoding Chimeric VEGF protein
US-10-343-825A-12

```

```

RESULT 11
US-09-918-995-1813
; Sequence 1813, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyscq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1813
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(475)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1813

```

Query Match	35.3%	Score 168.4;	DB 10;	Length 475;
Best Local Similarity	66.0%;	Pred. No. 4,2e-48;		
Matches 260;	Conservative 0;	Mismatches 131;	Indels 3;	Gaps 1
81	TGGGAACTCAACAGAAATGGAAGTGTGCTTTCAATGAAGTGTGGGCGCGAGCTA	140		
29	TTGGATCGCTCGTCCGAGGTGGAAGTGTACCTTCCAGGAAGTGTGGGCGCGAGCTA	88		
141	CTGCCGGCCAAATGGAGAACTGGTGTACATTGACAGATGAACACCTTAATGAAGTGTCTCA	200		
89	CTGCCGGCGCTGGAGAGGCTGGTGGACGTCTGTCCGAGTACCCGACGCGAGGTGGAGCA	148		

Query Match	30.9%;	Score 147.4;	DB 13;	Length 474;
Best Local Similarity	70.1%;	Pred. No. 9.7e-41;		
Matches 218;	Conservative 0;	Mismatches 81;	Indels 12;	Gaps 1;

QY	1	ATGTCGGCCATGAAGCTGTTCACTTGCTCTTCGCAGGTCCCTAGCTGGGTGCGTGTGCAC	60
Db	1	ATGCGGGTATGAGGCTGTTTCCCTTCCTCGAGCTCTCTGCGCGGGTGGCGGTGCGCT	60
QY	61	TCC-----CAGGGGGCCCTGTCTGTGGGAAACAACCTCAACAGAAATGGAAGTG	108
Db	61	GCTGTGCCCCCCCAGCAGTGGGGCTTGCTGTGGGAAAGCGTCTGTCAAGTGGGAAGTG	120
QY	109	GTGCTTTTCAATGAAGTGTGGGGCGCAGCTACTCGCGCCCAATGGAGAAGCTGTGTATC	168
Db	121	GTACCCCTTCAGGAAGTGTGGGGCGCAGCTACTGCGGGCGCTGGAGAGGCTGTGTGGAC	180
QY	169	ATTGCAGATGAACACCCATTAAGATGTTCTATATATTCAGTCCGTCATGTGTCTTCTG	228
Db	181	GTGCTGTCCGAGTACCCCGCAGGTGGAGCATGTTCCAGCCCATCTGTGTCTCCCTG	240
QY	229	AGTCCGTGTAGTGGCTGTGTGGTGACGAGGCTCTGCATCTGTGTGGCGCTAAAGACAGCC	288
Db	241	CTCGGCTGCACCGCTGTCTCGCGCATGAGATCTGCATGTATACAGCGTTCAAACACGA	300
QY	289	AACATCACTAT	299
Db	301	AATACAACCTGT	311

Db	259	GAGTCCACATCACCATGCGATTATTCGGGATCAAACTCCCAAGGCCAGCA---CATA	315
QY	343	GTGGAGATGACATTTCTCTCAGGATGTACTCTGCGAATGCGAGGCTATTCTGGAGACGACA	402
Db	316	GGAGAGATGAGCTTCTCTACAGCACAAATGTGAATGCAGACCAAGAGGATAGAGCA	375
QY	403	AAGGCAGAAAGGAGGAAACCAAGGGGAGAGGAAG	438
Db	376	AGACAGAGAAAAAATCAGTTTCAGGAGAAAGGAAG	411

Search completed: September 16, 2004, 22:22:40
 Job time : 350 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2004, 09:33:13 ; Search time 129 Seconds
(without alignments)

346.066 Million cell updates/sec

Title: US-10-071-370A-4

Perfect score: 846

Sequence: 1 MLAMKLTCTFLQVLAVLH.....RTKGRKRKSKTPQTEPHL 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	158	2	AAR27353 Sequence
2	846	100.0	158	2	AAR27357 Sequence
3	846	100.0	158	2	AAR22349 Rat VEGF
4	846	100.0	158	2	AAR22349 Rat VEGF
5	846	100.0	158	2	AAR22349 Rat VEGF
6	846	100.0	158	2	AAR22349 Rat VEGF
7	846	100.0	158	2	AAR22349 Rat VEGF
8	846	100.0	158	2	AAR22349 Rat VEGF
9	846	100.0	158	2	AAR22349 Rat VEGF
10	846	100.0	158	2	AAR22349 Rat VEGF
11	846	100.0	158	2	AAR22349 Rat VEGF
12	846	100.0	158	2	AAR22349 Rat VEGF
13	846	100.0	158	2	AAR22349 Rat VEGF
14	846	100.0	158	2	AAR22349 Rat VEGF
15	846	100.0	158	2	AAR22349 Rat VEGF
16	846	100.0	158	2	AAR22349 Rat VEGF
17	846	100.0	158	2	AAR22349 Rat VEGF
18	846	100.0	158	2	AAR22349 Rat VEGF
19	846	100.0	158	2	AAR22349 Rat VEGF
20	846	100.0	158	2	AAR22349 Rat VEGF
21	846	100.0	158	2	AAR22349 Rat VEGF
22	846	100.0	158	2	AAR22349 Rat VEGF
23	846	100.0	158	2	AAR22349 Rat VEGF
24	846	100.0	158	2	AAR22349 Rat VEGF
25	846	100.0	158	2	AAR22349 Rat VEGF

26	498.5	58.9	154	2	AAR27349
27	498.5	58.9	154	3	AAY57033
28	498.5	58.9	154	4	AAB37509
29	498.5	58.9	154	6	ADA25603
30	498.5	58.9	170	4	AAY97566
31	492.5	58.2	170	2	AAR23060
32	474.5	56.1	149	3	AAB10646
33	474.5	56.1	149	3	AAY57034
34	474.5	56.1	149	4	AAB37511
35	474.5	56.1	149	4	AAY97565
36	474.5	56.1	149	4	AAY97565
37	474.5	56.1	149	6	ABU03512
38	474.5	56.1	149	6	ADA25609
39	474.5	56.1	149	7	ADD08952
40	474.5	56.1	155	5	ABB06756
41	465.5	55.0	149	2	AAR23059
42	456.5	54.0	170	2	AAR86204
43	448.5	53.0	152	2	AAY08289
44	416.5	49.2	131	2	AAY08288
45	365.5	43.2	163	5	ABB06757

ALIGNMENTS

RESULT 1

AAR27353

ID AAR27353 standard; protein; 158 AA.

XX AC AAR27353;

XX DT 25-MAR-2003 (revised)

DT 25-FEB-1993 (first entry)

XX DE Sequence of vascular endothelial cell growth factor VEGF AB subunit B.

XX KW Vascular development; mitogen; blood vessel;

XX KW vascular endothelial growth factor; neovascularisation.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 97

FT FT /label= glycosylation site

XX PN EP506477-A1.

XX PD 30-SEP-1992.

XX PF 27-MAR-1992; 92EP-00302750.

XX PR 28-MAR-1991; 91US-00676436.

XX PA (MERI) MERCK & CO INC.

XX PT Bayne ML, Thomas KA;

XX PT WPI; 1992-325745/40.

XX PT N-PSDB; AAQ28952.

XX PT Vascular endothelial cell growth factor sub-units - which stimulate

XX PT vascular endothelial cell growth, used for inducing tissue repair and

XX PS Example; Fig 3; 61pp; English.

XX CC GS-9L cells were cultured and the VEGF AB subunits were isolated and

XX CC sequenced. The reduced and carboxymethylated protein eluted as two peaks

XX CC at approx. 23 and 25 ml that were of approx. equal area as determined by

XX CC monitoring absorbance at 210 nm. Samples of the two protein subunits

XX CC isolated after reduction and carboxymethylation were each applied to

XX CC polybrene-coated glass fiber filters and their N-terminal sequences were

XX CC determined. The peak of absorbance eluting at approx 25 ml (A subunit)

CC yielded an amino terminal sequence Ala Pro Thr Glu Gly Glu Lys Ala
 CC His Glu Val identical to VEGF AA. The peak of absorbance eluting at
 CC approx. 23 ml (B subunit) yielded the N-terminal sequence Ala Leu Ser Ala
 CC Gly Asn Xaa Ser Thr Glu Met Glu Val Val Pro Phe Asn Glu Val plus a nearly
 CC equal amount of a truncated form of the same sequence missing the first
 CC three residues. The missing X residue corresp. to an Asn in the cloned
 CC sequence. The A and sum of the B chain peptides were recovered in nearly
 CC equal amounts supporting the interpretation that the two peptides
 CC combine to form an AB heterodimer in VEGF II. The form of VEGF AB mature
 CC A subunit in the heterodimer is the 164 amino acid form. The form of VEGF
 CC AB mature B subunit in the heterodimer is the 135 amino acid form derived
 CC from the 158 full length amino acid form. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)
 XX
 SQ Sequence 158 AA;

Query Match 100.0%; Score 846; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAMKLFCTCFLQVLAVHSQALSGAGNNSTEMEVVPPNEVNGRSYCRPMKLVYIADE 60
 DB 1 MLAMKLFCTCFLQVLAVHSQALSGAGNNSTEMEVVPPNEVNGRSYCRPMKLVYIADE 60
 QY 61 HNEVSHIFSPSCVLLSRCSCGCCGDEGLHCVALKTANITMQILKIPPNRDPHSYVEMTFS 120
 DB 61 HNEVSHIFSPSCVLLSRCSCGCCGDEGLHCVALKTANITMQILKIPPNRDPHSYVEMTFS 120
 QY 121 QDVLCRCRPILETTKAERRKTKGKRKQSKTPTQTEPHL 158
 DB 121 QDVLCRCRPILETTKAERRKTKGKRKQSKTPTQTEPHL 158

RESULT 2
 AAR27357
 ID AAR27357 standard; protein; 158 AA.

XX AAR27357;
 AC
 XX
 DT 25-MAR-2003 (revised)
 DT 25-FEB-1993 (first entry)
 XX
 DE Sequence of vascular endothelial cell growth factor VEGF B 158 amino acid
 DE residue subunit.
 KW Vascular development; mitogen; blood vessel;
 KW vascular endothelial growth factor; neovascularisation.
 XX
 OS Rattus.
 XX EP506477-A1.
 XX
 XX 30-SEP-1992.
 XX
 PF 27-MAR-1992; 92BP-00302750.
 XX
 XX 28-MAR-1991; 91US-00676436.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Bayne ML, Thomas KA;
 PI WPI; 1992-325745/40.
 XX N-PSDB; AAQ28956.
 DR
 DR Vascular endothelial cell growth factor sub-units - which stimulate
 PT vascular endothelial cell growth, used for inducing tissue repair and
 PT growth.
 PT
 XX
 XX Disclosure; Fig 8; 61pp; English.
 PS
 CC The full length coding region of the B subunit or monomer of VEGF is
 CC determined from four sets of overlapping cDNA clones. Degenerate oligo.

CC primers based on the amino acid sequences from polypeptide L50 are used
 CC to PCR amplify the central region of the cDNA for VEGF AB,B monomer. A
 CC single band migrating at 108 bp was gel purified, digested with SalI,
 CC ligated into pGEM3Zf(+) and sequenced. The nucleotide sequence obtained
 CC (pIG) was used to design antisense and sense PCR primers to amplify the
 CC 5' and 3' ends of the cDNA. These 5' and 3' clones are denoted p5V2 and
 CC p3V2 respectively. The entire base sequence for the 158 amino acid
 CC microheterogeneous B subunit and the 138 amino acid microheterogeneous B
 CC subunit are shown in AAQ28955 and AAQ28956. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)
 XX
 SQ Sequence 158 AA;

Query Match 100.0%; Score 846; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAMKLFCTCFLQVLAVHSQALSGAGNNSTEMEVVPPNEVNGRSYCRPMKLVYIADE 60
 DB 1 MLAMKLFCTCFLQVLAVHSQALSGAGNNSTEMEVVPPNEVNGRSYCRPMKLVYIADE 60
 QY 61 HNEVSHIFSPSCVLLSRCSCGCCGDEGLHCVALKTANITMQILKIPPNRDPHSYVEMTFS 120
 DB 61 HNEVSHIFSPSCVLLSRCSCGCCGDEGLHCVALKTANITMQILKIPPNRDPHSYVEMTFS 120
 QY 121 QDVLCRCRPILETTKAERRKTKGKRKQSKTPTQTEPHL 158
 DB 121 QDVLCRCRPILETTKAERRKTKGKRKQSKTPTQTEPHL 158

RESULT 3
 AAR22349
 ID AAR22349 standard; protein; 158 AA.

XX AAR22349;
 AC
 XX
 DT 29-JUL-1992 (first entry)
 DT
 DE Rat VEGF-II 135 amino acid mature B-subunit.
 XX
 KW VEGF-II; mammalian glioma cell; conditioned medium; heterodimer;
 KW homodimer; mitogenesis; vascular repair; blood vessel implant.
 XX
 OS Rattus.
 XX
 XX Key
 FH Location/Qualifiers
 FT Peptide
 FT /label= signal
 FT Protein
 FT /label= mature_VEGF_B_monomer
 FT Peptide
 FT /label= [L44]
 FT /note= "Leu C cleavage peptide"
 FT Modified-site
 FT /label= N-glycosylation
 FT Peptide
 FT /label= L50
 FT /note= "Leu C cleavage peptide"
 FT Peptide
 FT /label= L35
 FT /note= "Leu C cleavage peptide"
 FT Modified-site
 FT /label= N-glycosylation
 FT Peptide
 FT /label= [L44]
 FT /note= "Leu C cleavage peptide"
 FT Peptide
 FT /label= L26
 FT /note= "Leu C cleavage peptide"
 XX
 XX EP476983-A.
 XX
 PD 25-MAR-1992.

XX 18-SEP-1991; 91EP-00308489.
 XX 21-SEP-1990; 90US-00586638.
 XX 21-SEP-1990; 90US-00586640.
 XX (MERI) MERCK & CO INC.
 XX Bayne ML, Conn GL, Thomas KA;
 XX WPI: 1992-098641/13.
 XX N-PSDB; AAQ23040.
 XX Vascular endothelial cell growth factor II - used as coating for
 XX artificial blood vessels or to promote tissue repair.
 XX Claim 8; Fig 6; 38pp; English.
 XX The full-length coding region of the B monomer was determined from four
 XX sets of overlapping cDNA clones. PCR primers were designed based on the
 XX amino acid sequence of a Leu C peptide (150) and used to amplify the
 XX central region of the cDNA. A single band migrating at 108bp was gel
 XX purified, digested with SalI, ligated into pGEM3Zf(+) and sequenced. The
 XX nucleotide sequence obtained was used to design antisense and sense PCR
 XX primers to amplify the 5' and 3' ends of the cDNA and complete the full-
 XX length sequence. The VEGF-II can exist as a homodimer or as a heterodimer
 XX with an A-subunit (see AAR22347). VEGF-II can be used to stimulate
 XX endothelial cells for induction of blood vessel growth, for vascular
 XX repair and for production of artificial blood vessels. See also AAQ23038
 XX and AAQ23041-Q23059
 XX SQ Sequence 158 AA;
 XX Query Match 100.0%; Score 846; DB 2; Length 158;
 XX Best Local Similarity 100.0%; Pred. No. 4e-86;
 XX Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAMKLFCTCFLQVLAVHSQGLSAGNNSSTEMEVVFNFWGRCYCRPMEKLVYIADE 60
 DB 1 MLAMKLFCTCFLQVLAVHSQGLSAGNNSSTEMEVVFNFWGRCYCRPMEKLVYIADE 60
 QY 61 HPNEVSHIPSPSCVLLSRCSGCCGDEGLHCVALKTANITMQILKIPNDRDPHSYVENTFS 120
 DB 61 HPNEVSHIPSPSCVLLSRCSGCCGDEGLHCVALKTANITMQILKIPNDRDPHSYVENTFS 120
 QY 121 QDVLCERPILETTKAERRKTGKQSKTPTQTEPHL 158
 DB 121 QDVLCERPILETTKAERRKTGKQSKTPTQTEPHL 158
 RESULT 5
 AAWS3646
 ID AAWS3644 standard; protein; 158 AA.
 XX AAWS3644;
 XX 30-JUL-1998 (first entry)
 XX Vascular endothelial growth factor II A subunit 3.
 XX Vascular endothelial cell growth factor; VEGF II; rat; glioma cell;
 XX mitogenesis; blood vessel growth; artificial blood vessel.
 XX Rattus sp.
 XX US5726152-A.
 XX 10-MAR-1998.
 XX 31-AUG-1994; 94US-00299185.
 XX 21-SEP-1990; 90US-00586638.
 XX 05-JAN-1993; 93US-00000834.
 XX (MERI) MERCK & CO INC.
 XX Conn GL, Thomas KA, Bayne ML;
 XX WPI: 1998-206007/18.
 XX N-PSDB; AAQ25538.
 XX Vascular endothelial growth factor proteins - having specified A and B
 XX sub-units.

XX Claim 1; Fig 6; 46pp; English.

XX The present sequence represents a rat vascular endothelial growth factor

CC II (VEGF II) B subunit. The present invention describes: (1) a mammalian

CC VEGF II protein comprising an A subunit from AAW53639, AAW53640 or

CC AAW53641, and a B subunit from AAW53638, AAW53639 or the first 135-135

CC amino acids of AAW53638; and (2) a mammalian VEGF comprising a

CC heterodimer or homodimer of B subunits. The growth factor is used for

CC promoting vascular development and repair and for promoting tissue repair

XX Sequence 158 AA;

SQ

Query Match 100.0%; Score 846; DB 2; Length 158;

Best Local Similarity 100.0%; Pred. No. 4e-86;

Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTFCFLOVLAVHSQALSGAGNNSTEMEVVPPNEVWGRSYCRPMKLVVIAD 60

DB 1 MLAMKLTFCFLOVLAVHSQALSGAGNNSTEMEVVPPNEVWGRSYCRPMKLVVIAD 60

QY 61 HPNEVSHIFSPSCVLLSRCSCGCCGDEGLHCVALKTANITWQILKIPPNRDPHSYVEMTFS 120

DB 61 HPNEVSHIFSPSCVLLSRCSCGCCGDEGLHCVALKTANITWQILKIPPNRDPHSYVEMTFS 120

QY 121 QDVLCRCRILETTKAERRKTGKRKQSKTPQTEEPHL 158

DB 121 QDVLCRCRILETTKAERRKTGKRKQSKTPQTEEPHL 158

RESULT 6

AAV57032

ID AAY57032 standard; protein; 158 AA.

XX AAY57032;

XX 15-FEB-2000 (first entry)

XX VEGFB 158 amino acid residue subunit sequence.

DE VEGF; vascular endothelial growth factor; B subunit; tissue growth;

XX vascular development; artificial blood vessel; repair; human.

XX Homo sapiens.

XX US5994300-A.

XX 30-NOV-1999.

XX 20-SEP-1993; 93US-00124259.

XX 28-MAR-1991; 91US-00676436.

XX (MERI) MERCK & CO INC.

XX Thomas KA, Bayne ML;

XX WPI; 2000-038268/03.

XX N-PSDB; AA239830.

XX Purified and isolated vascular endothelial cell growth factor C subunit

PT for the induction of tissue repair or growth.

XX Disclosure; Fig 8; 58pp; English.

XX This is the amino acid sequence of a 158 amino acid residue B subunit of

CC vascular endothelial cell growth factor (VEGF). The invention relates to

CC a purified and isolated VEGF C subunit amino acid sequence AAY57025. VEGF

CC exists in various microheterogeneous forms, and is useful for the

CC promotion of vascular development and repair. The invention also relates

CC to human VEGF heterodimers AC or BC and homodimer CC, where A, B and C

CC are subunit amino acid sequences. The VEGF AC, BC or CC amino acid

CC sequences can be used in a tissue repairing pharmaceutical composition.

CC The novel growth factors are useful for the production or coverage of

CC artificial blood vessels with vascular endothelial cell. They are also

CC useful for the induction of tissue growth and repair

XX Sequence 158 AA;

SQ

Query Match 100.0%; Score 846; DB 3; Length 158;

Best Local Similarity 100.0%; Pred. No. 4e-86;

Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTFCFLOVLAVHSQALSGAGNNSTEMEVVPPNEVWGRSYCRPMKLVVIAD 60

DB 1 MLAMKLTFCFLOVLAVHSQALSGAGNNSTEMEVVPPNEVWGRSYCRPMKLVVIAD 60

QY 61 HPNEVSHIFSPSCVLLSRCSCGCCGDEGLHCVALKTANITWQILKIPPNRDPHSYVEMTFS 120

DB 61 HPNEVSHIFSPSCVLLSRCSCGCCGDEGLHCVALKTANITWQILKIPPNRDPHSYVEMTFS 120

QY 121 QDVLCRCRILETTKAERRKTGKRKQSKTPQTEEPHL 158

DB 121 QDVLCRCRILETTKAERRKTGKRKQSKTPQTEEPHL 158

RESULT 7

AAV37508

ID AAB37508 standard; protein; 158 AA.

XX AAB37508;

XX 26-FEB-2001 (first entry)

XX Rat VEGF subunit B SEQ ID NO: 39.

DE Vascular endothelial growth factor; VEGF C subunit; cell division;

XX artificial blood vessel; tissue growth; tissue repair.

XX Rattus sp.

XX US6140073-A.

XX 31-OCT-2000.

XX 16-JAN-1996; 96US-00586039.

XX 28-MAR-1991; 91US-00676436.

XX 20-SEP-1993; 93US-00124259.

XX (MERI) MERCK & CO INC.

XX Thomas KA, Bayne ML;

XX WPI; 2001-014858/02.

XX N-PSDB; AAC83515.

XX Human vascular endothelial cell growth factor (VEGF) C subunit DNA and

PT protein, useful for promoting vascular development and repair, and for

PT promoting tissue repair, especially for treating wounds in mammals.

XX Example 10; Fig 8; 58pp; English.

XX The present invention is concerned with the human vascular endothelial

CC growth factor (VEGF) C subunit. VEGF is a vascular endothelial cell

CC mitogen and can be used to promote vascular development and repair. The C

CC subunit may exist as a homodimer or a heterodimer with the VEGF A or B

CC subunit. VEGF can be used in the treatment of wounds of mammals, to cover

CC artificial blood vessels with vascular endothelial cells, in the

CC production of artificial blood vessels and to induce tissue repair or

CC growth

XX Sequence 158 AA;

SQ

Query Match 100.0%; Score 846; DB 4; Length 158;

Best Local Similarity 100.0%; Pred. No. 4e-86;

Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTCTCFLQVLAVHSQGLSAGNNSSTEMEVFPNEVWGRSYCRPMKLVYIADE 60
 DB 1 MLAMKLTCTCFLQVLAVHSQGLSAGNNSSTEMEVFPNEVWGRSYCRPMKLVYIADE 60
 QY 61 HPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTANITWQILKIPNRPDHSYVENTFS 120
 DB 61 HPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTANITWQILKIPNRPDHSYVENTFS 120

QY 121 QDVLCECRPILETTKARRTKGKRKQSKTPQTEEPHL 158
 DB 121 QDVLCECRPILETTKARRTKGKRKQSKTPQTEEPHL 158

RESULT 8
 AAB73963
 ID AAB73963 standard; protein; 158 AA.
 XX
 AC AAB73963;
 XX
 DT 23-NOV-2001 (first entry)
 XX
 DE Rat VEGF I B subunit.
 XX
 KW Rat; vascular endothelial growth factor II; VEGF-II; wound healing;
 KW vascular repair; neovascularisation; tissue repair; VEGF I B subunit;
 KW vulnery; angiogenesis.
 XX
 OS Rattus sp.
 XX
 XX US6180107-B1.
 XX
 XX 30-JAN-2001.
 XX
 XX 10-MAR-1998; 98US-00038199.
 XX
 XX 21-SEP-1990; 90US-00586638.
 PR 05-JAN-1993; 93US-00000834.
 PR 31-AUG-1994; 94US-00299185.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Bayne ML, Conn GL, Thomas KA;
 XX
 XX WPI; 2001-256064/26.
 DR N-PSDB; AAF81272.
 XX
 XX Stimulating angiogenesis or wound healing through vascular repair,
 PT neovascularization or both, comprises administering mammalian vascular
 PT endothelial growth factor II comprising two different subunits.
 XX
 PS Disclosure; Fig 4I-4K; 46pp; English.
 XX
 XX The invention relates to a method for stimulating angiogenesis or wound
 CC healing through vascular repair, neovascularisation or both. The method
 CC comprises administering to a patient a pharmaceutically effective amount
 CC of mammalian vascular endothelial growth factor II (VEGF-II) comprising a
 CC heterodimer of subunits A and B, or a homodimer of B subunits. VEGF-II is
 CC useful for vascular development and repair, promotion of tissue repair,
 CC and the production of artificial vessels. The present sequence is VEGF I
 CC B subunit
 XX
 SQ Sequence 158 AA;

Query Match 100.0%; Score 846; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTCTCFLQVLAVHSQGLSAGNNSSTEMEVFPNEVWGRSYCRPMKLVYIADE 60
 DB 1 MLAMKLTCTCFLQVLAVHSQGLSAGNNSSTEMEVFPNEVWGRSYCRPMKLVYIADE 60

QY 61 HPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTANITWQILKIPNRPDHSYVENTFS 120
 DB 61 HPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTANITWQILKIPNRPDHSYVENTFS 120

QY 121 QDVLCECRPILETTKARRTKGKRKQSKTPQTEEPHL 158
 DB 121 QDVLCECRPILETTKARRTKGKRKQSKTPQTEEPHL 158

RESULT 9
 AAB73964
 ID AAB73964 standard; protein; 158 AA.
 XX
 AC AAB73964;
 XX
 DT 23-NOV-2001 (first entry)
 XX
 DE Rat VEGF II B subunit mature 135 amino acid form.
 XX
 KW Rat; vascular endothelial growth factor II; VEGF-II; wound healing;
 KW vascular repair; neovascularisation; tissue repair; VEGF II B subunit;
 KW vulnery; angiogenesis.
 XX
 OS Rattus sp.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1. .23
 FT /label= Signal_peptide
 FT Protein 24. .158
 FT /label= VEGF_II_B_subunit
 XX
 XX US6180107-B1.
 XX
 XX 30-JAN-2001.
 XX
 XX 10-MAR-1998; 98US-00038199.
 XX
 XX 21-SEP-1990; 90US-00586638.
 PR 05-JAN-1993; 93US-00000834.
 PR 31-AUG-1994; 94US-00299185.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Bayne ML, Conn GL, Thomas KA;
 XX
 XX WPI; 2001-256064/26.
 DR N-PSDB; AAF81273.
 XX
 XX Stimulating angiogenesis or wound healing through vascular repair,
 PT neovascularization or both, comprises administering mammalian vascular
 PT endothelial growth factor II comprising two different subunits.
 XX
 PS Claim 1; Fig 6; 46pp; English.
 XX
 XX The invention relates to a method for stimulating angiogenesis or wound
 CC healing through vascular repair, neovascularisation or both. The method
 CC comprises administering to a patient a pharmaceutically effective amount
 CC of mammalian vascular endothelial growth factor II (VEGF-II) comprising a
 CC heterodimer of subunits A and B, or a homodimer of B subunits. VEGF-II is
 CC useful for vascular development and repair, promotion of tissue repair,
 CC and the production of artificial vessels. The present sequence is the
 CC mature 135 amino acid form of VEGF II B subunit
 XX
 SQ Sequence 158 AA;

Query Match 100.0%; Score 846; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTCTCFLQVLAVHSQGLSAGNNSSTEMEVFPNEVWGRSYCRPMKLVYIADE 60
 DB 1 MLAMKLTCTCFLQVLAVHSQGLSAGNNSSTEMEVFPNEVWGRSYCRPMKLVYIADE 60

QY 61 HPNEVSHIFSPSCVLLSRCSGCCDEGLHCVALKTANITMQLIKIPNRPDPSHVEMTFS 120
 Db 61 HPNEVSHIFSPSCVLLSRCSGCCDEGLHCVALKTANITMQLIKIPNRPDPSHVEMTFS 120
 QY 121 QDVLCECRPILETTKAERRTKGKRKQSKTPQTEEPHL 158
 Db 121 QDVLCECRPILETTKAERRTKGKRKQSKTPQTEEPHL 158

RESULT 10
 ABU62003
 ID ABU62003 standard; protein; 158 AA.
 XX
 AC ABU62003;
 XX
 DT 19-AUG-2003 (first entry)
 XX
 DE Amino acid sequence for rat VEGF I A subunit cleavage product #2.
 DE
 KW Rat; vascular endothelial growth factor II; VEGF II; mitogenesis;
 KW mammalian; vascular endothelial cell growth; tissue repair;
 KW vascular development; vascular repair; blood vessel growth;
 KW neovascularisation; artificial blood vessel; polymeric vessel; vulnery;
 KW A subunit.
 XX
 OS Rattus sp.

XX
 FH Key
 FT Peptide 1..23 Location/Qualifiers
 FT Protein 24..158 /label= Signal_peptide
 FT /label= Mature_secreted_VEGF_I_A_subunit
 XX US2003045471-A1.
 XX
 XX 06-MAR-2003.
 XX
 XX 08-FEB-2002; 2002US-00071370.
 XX
 XX 21-SEP-1990; 90US-00586638.
 XX 05-JAN-1993; 93US-00000834.
 XX 31-AUG-1994; 94US-00299185.
 XX 10-MAR-1998; 98US-00038199.
 XX 07-JUN-1999; 99US-00326879.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Bayne ML, Conn GL, Thomas KA;
 XX
 XX WPI: 2003-371473/35.
 XX N-PSDB; ACA62371.
 XX
 XX New heterodimeric vascular endothelial growth factor II comprising A and
 XX B subunits encoded by different genes, useful for preparing a composition
 XX for promoting vascular or tissue repair or neovascularization.
 XX
 XX Example 9; Fig 4I-4K; 50pp; English.

XX
 CC The present invention relates to the isolation of vascular endothelial
 CC growth factor II (VEGF II), and the polynucleotide sequences encoding it.
 CC VEGF II is a heterodimer comprising A and B subunits that are encoded by
 CC different genes. VEGF II stimulates mitogenesis of mammalian vascular
 CC endothelial cells. VEGF II is useful for promoting tissue repair and for
 CC stimulating the growth of vascular endothelial cells. VEGF II can also be
 CC used for stimulating the growth of vascular endothelial cells in a
 CC patient to promote vascular development and repair, or blood vessel
 CC growth (neovascularisation). VEGF II can further be used to produce
 CC artificial blood vessels by treating synthetic polymeric vessels with
 CC VEGF II, and implanting into them into a patient. After the implantation
 CC endothelial cells migrate into and grow on the artificial surface. The
 CC present sequence represents rat VEGF I A subunit cleavage product #2
 XX
 XX Sequence 158 AA;

Query Match 100.0%; Score 846; DB 6; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAMKLTCTCFLQVLAHVSQAGSAGNNSTEMEVVPPFNEVWGRSYCRPMKLVYIADE 60
 Db 1 MLAMKLTCTCFLQVLAHVSQAGSAGNNSTEMEVVPPFNEVWGRSYCRPMKLVYIADE 60
 QY 61 HPNEVSHIFSPSCVLLSRCSGCCDEGLHCVALKTANITMQLIKIPNRPDPSHVEMTFS 120
 Db 61 HPNEVSHIFSPSCVLLSRCSGCCDEGLHCVALKTANITMQLIKIPNRPDPSHVEMTFS 120
 QY 121 QDVLCECRPILETTKAERRTKGKRKQSKTPQTEEPHL 158
 Db 121 QDVLCECRPILETTKAERRTKGKRKQSKTPQTEEPHL 158

RESULT 11
 ABU62006
 ID ABU62006 standard; protein; 158 AA.
 XX
 AC ABU62006;
 XX
 DT 19-AUG-2003 (first entry)
 XX
 DE Amino acid sequence for rat VEGF II B subunit.
 DE
 KW Rat; vascular endothelial growth factor II; VEGF II; mitogenesis;
 KW mammalian; vascular endothelial cell growth; tissue repair;
 KW vascular development; vascular repair; blood vessel growth;
 KW neovascularisation; artificial blood vessel; polymeric vessel; vulnery;
 KW B subunit.
 XX
 OS Rattus sp.

XX
 FH Key
 FT Peptide 1..23 Location/Qualifiers
 FT Protein 24..158 /label= Signal_peptide
 FT /label= Mature_secreted_VEGF_II_B_subunit
 XX US2003045471-A1.
 XX
 XX 06-MAR-2003.
 XX
 XX 08-FEB-2002; 2002US-00071370.
 XX
 XX 21-SEP-1990; 90US-00586638.
 XX 05-JAN-1993; 93US-00000834.
 XX 31-AUG-1994; 94US-00299185.
 XX 10-MAR-1998; 98US-00038199.
 XX 07-JUN-1999; 99US-00326879.
 XX
 XX (MERI) MERCK & CO INC.

XX
 PI Bayne ML, Conn GL, Thomas KA;
 XX
 XX WPI: 2003-371473/35.
 XX N-PSDB; ACA62374.
 XX
 XX New heterodimeric vascular endothelial growth factor II comprising A and
 XX B subunits encoded by different genes, useful for preparing a composition
 XX for promoting vascular or tissue repair or neovascularization.
 XX
 XX Claim 6; Fig 6; 50pp; English.
 XX
 CC The present invention relates to the isolation of vascular endothelial
 CC growth factor II (VEGF II), and the polynucleotide sequences encoding it.
 CC VEGF II is a heterodimer comprising A and B subunits that are encoded by
 CC different genes. VEGF II stimulates mitogenesis of mammalian vascular
 CC endothelial cells. VEGF II is useful for promoting tissue repair and for
 CC stimulating the growth of vascular endothelial cells. VEGF II can also be
 XX

CC used for stimulating the growth of vascular endothelial cells in a
 CC patient to promote vascular development and repair, or blood vessel
 CC growth (neovascularisation). VEGF II can further be used to produce
 CC artificial blood vessels by treating synthetic polymeric vessels with
 CC VEGF II and implanting into them into a patient. After the implantation
 CC endothelial cells migrate into and grow on the artificial surface. The
 CC present sequence represents rat VEGF II B subunit

SQ Sequence 158 AA;
 Query Match 100.0%; Score 846; DB 6; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAMKLTFCFLOVLAVHSQGLSAGNNSNSTEMEVVFNVEVWGRSYCRPMKLVYIADE 60
 DB 1 MLAMKLTFCFLOVLAVHSQGLSAGNNSNSTEMEVVFNVEVWGRSYCRPMKLVYIADE 60
 QY 61 HPNEVSHIFSPSCVLLSRGCGCGDEGLHCVALKTANITMQILKIPNDRPHSVEMTFS 120
 DB 61 HPNEVSHIFSPSCVLLSRGCGCGDEGLHCVALKTANITMQILKIPNDRPHSVEMTFS 120
 QY 121 QDVLCRCRPILETTKAERRKTGKRKQSKTPQTEPHL 158
 DB 121 QDVLCRCRPILETTKAERRKTGKRKQSKTPQTEPHL 158

RESULT 12
 ADA25601
 ID ADA25601 standard; protein; 158 AA.
 XX
 AC ADA25601;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Rat VEGF B 158 amino acid subunit.
 XX
 KW Vascular endothelial cell growth;
 KW VEGF-A; VEGF-B; VEGF-C;
 KW mitogen; vascular development; vascular repair; tissue development;
 KW tissue repair; rat.
 XX
 OS Rattus sp.
 XX
 PN US569434-B1.
 XX
 PD 27-MAY-2003.
 XX
 PF 30-OCT-2000; 2000US-00699769.
 XX
 PR 28-MAR-1991; 91US-00676436.
 PR 20-SEP-1993; 93US-00124259.
 PR 16-JAN-1996; 96US-00586039.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Bayne ML, Thomas KA;
 XX
 DR WPI; 2003-605461/57.
 DR N-PSDB; ADA25600.

Stimulating vascular endothelial cell growth comprises administering an amount of a vascular endothelial cell growth factor comprising a first and a second C subunit amino acid sequence.

Example 10; Fig 8; 58pp; English.

The invention relates to stimulating vascular endothelial cell growth comprises administering to a patient an effective vascular endothelial stimulatory amount of a vascular endothelial cell growth factor (VEGF) comprising a first and a second C subunit amino acid sequence, where the first and second subunits comprise a sequence appearing as ADA25607. Also disclosed as new are rat VEGF-A, -B and C subunit cDNAs and proteins. The

CC method and VEGF (a mitogen) are useful in inducing vascular or tissue development and repair. The present sequence represents a rat VEGF subunit.

SQ Sequence 158 AA;

Query Match 100.0%; Score 846; DB 6; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTFCFLOVLAVHSQGLSAGNNSNSTEMEVVFNVEVWGRSYCRPMKLVYIADE 60
 DB 1 MLAMKLTFCFLOVLAVHSQGLSAGNNSNSTEMEVVFNVEVWGRSYCRPMKLVYIADE 60
 QY 61 HPNEVSHIFSPSCVLLSRGCGCGDEGLHCVALKTANITMQILKIPNDRPHSVEMTFS 120
 DB 61 HPNEVSHIFSPSCVLLSRGCGCGDEGLHCVALKTANITMQILKIPNDRPHSVEMTFS 120
 QY 121 QDVLCRCRPILETTKAERRKTGKRKQSKTPQTEPHL 158
 DB 121 QDVLCRCRPILETTKAERRKTGKRKQSKTPQTEPHL 158

RESULT 13
 AAR27356
 ID AAR27356 standard; protein; 138 AA.
 XX
 AC AAR27356;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-FEB-1993 (first entry)
 XX
 DE Sequence of vascular endothelial cell growth factor VEGF B 138 amino acid residue subunit.
 XX
 KW Vascular development; mitogen; blood vessel;
 KW vascular endothelial growth factor; neovascularisation.
 XX
 OS Rattus.
 XX
 PN EP506477-A1.
 XX
 PD 30-SEP-1992.
 XX
 PF 27-MAR-1992; 92EP-00302750.
 XX
 PR 28-MAR-1991; 91US-00676436.
 XX
 PA (MERI) MERCK & CO INC.

Bayne ML, Thomas KA;
 WPI; 1992-325745/40.
 N-PSDB; AAQ28955.
 Vascular endothelial cell growth factor sub-units - which stimulate vascular endothelial cell growth, used for inducing tissue repair and growth.

Disclosure; Fig 7; 61pp; English.

The full length coding region of the B subunit or monomer of VEGF is determined from four sets of overlapping cDNA clones. Degenerate oligo. primers based on the amino acid sequences from polypeptide L50 are used to PCR amplify the central region of the cDNA for VEGF AB, B monomer. A single band migrating at 108 bp was gel purified, digested with SalI, ligated into pGEM3zf(+) and sequenced. The nucleotide sequence obtained (pVG) was used to design antisense and sense PCR primers to amplify the 5' and 3' ends of the cDNA. These 5' and 3' clones are denoted p5V2 and p3V2 respectively. The entire base sequence for the 158 amino acid microheterogeneous B subunit and the 138 amino acid microheterogeneous B subunit are shown in AAQ28955 and AAQ28956. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)

```

XX SQ Sequence 138 AA;
Query Match 87.5%; Score 740; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.3e-74;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTFCFLQVLAVHSQGLSAGNNSSTEMEVVFNVEVGRSYCRPMKLVYIADE 60
Db 1 MLAMKLTFCFLQVLAVHSQGLSAGNNSSTEMEVVFNVEVGRSYCRPMKLVYIADE 60
QY 61 HPNEVSHIFSPSCVLLSRSCGCCDEGLHCVALKTANITMQLKIPNRPDHSYVENTFS 120
Db 61 HPNEVSHIFSPSCVLLSRSCGCCDEGLHCVALKTANITMQLKIPNRPDHSYVENTFS 120
QY 121 QDVLCECRPILETTKAER 138
Db 121 QDVLCECRPILETTKAER 138

RESULT 14
AAR22350
ID AAR22350 standard; protein; 138 AA.
XX AC AAR22350;
XX DT 29-JUL-1992 (first entry)
XX DE Rat VEGF-II 115 amino acid mature B-subunit.
XX KW VEGF-II; mammalian glioma cell; conditioned medium; heterodimer;
XX OS homodimer; mitogenesis; vascular repair; blood vessel implant.
XX FH Rattus.
XX Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
FT Protein 24..138
FT /label= mature_VEGF_B_monomer
FT Modified-site 30..32
FT /label= N-glycosylation
FT Modified-site 97..99
FT /label= N-glycosylation
XX EP476983-A.
XX PD 25-MAR-1992.
XX PF 18-SEP-1991; 91EP-00308489.
XX PR 21-SEP-1990; 90US-00586638.
XX PR 21-SEP-1990; 90US-00586640.
XX PA (MERI ) MERCK & CO INC.
XX PI Bayne ML, Conn GL, Thomas KA;
XX WPI; 1992-098641/13.
XX DR N-PSDB; AAR23040.
XX PT Vascular endothelial cell growth factor II - used as coating for
XX PT artificial blood vessels or to promote tissue repair.
XX PS Claim 8; Fig 6; 38pp; English.
XX CC The VEGF-II B-subunit exists in two forms; the mature protein has either
CC 135 or 115 amino acids. The two forms are generated by alternative
CC splicing of the mRNA transcript prior to translation. The proteins can be
CC isolated from glioma cell-conditioned medium. For example, the rat cell
CC line GS-9L was grown to confluence in MEM. VEGF-II was purified from the
CC conditioned medium by carboxymethyl-Sephadex chromatography, polyaspartic
CC acid WCX HPLC cation exchange chromatography, metal chelate

CC Chromatography and reverse phase chromatography. See also AAR23038,
CC AAR23040 and AAR23042-Q23059
XX SQ Sequence 138 AA;
Query Match 87.5%; Score 740; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.3e-74;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTFCFLQVLAVHSQGLSAGNNSSTEMEVVFNVEVGRSYCRPMKLVYIADE 60
Db 1 MLAMKLTFCFLQVLAVHSQGLSAGNNSSTEMEVVFNVEVGRSYCRPMKLVYIADE 60
QY 61 HPNEVSHIFSPSCVLLSRSCGCCDEGLHCVALKTANITMQLKIPNRPDHSYVENTFS 120
Db 61 HPNEVSHIFSPSCVLLSRSCGCCDEGLHCVALKTANITMQLKIPNRPDHSYVENTFS 120
QY 121 QDVLCECRPILETTKAER 138
Db 121 QDVLCECRPILETTKAER 138

RESULT 15
AAW53645
ID AAW53645 standard; protein; 138 AA.
XX AC AAW53645;
XX DT 30-JUL-1998 (first entry)
XX DE Vascular endothelial growth factor I A subunit 4.
XX KW Vascular endothelial cell growth factor; VEGF II; rat; glioma cell;
XX OS mitogenesis; blood vessel growth; artificial blood vessel.
XX FH Rattus sp.
XX OS US5726152-A.
XX PN 10-MAR-1998.
XX PD 31-AUG-1994; 94US-00299185.
XX PF 21-SEP-1990; 90US-00586638.
XX PR 05-JAN-1993; 93US-00000834.
XX PA (MERI ) MERCK & CO INC.
XX PI Conn GL, Thomas KA, Bayne ML;
XX WPI; 1998-206007/18.
XX DR N-PSDB; AAV25537.
XX PT Vascular endothelial growth factor proteins - having specified A and B
XX PT sub-units.
XX PS Example 9; Fig 4; 46pp; English.
XX CC The present sequence represents a rat vascular endothelial growth factor
XX CC I (VEGF I) A subunit. The present invention describes: (1) a mammalian
XX CC VEGF II protein comprising an A subunit from AAW53639, AAW53640 or
XX CC AAW53641, and a B subunit from AAW53638, AAW53639 or the first 115-135
XX CC amino acids of AAW53638; and (2) a mammalian VEGF comprising a
XX CC heterodimer or homodimer of B subunits. The growth factor is used for
XX CC promoting vascular development and repair and for promoting tissue repair
XX CC Sequence 138 AA;
Query Match 87.5%; Score 740; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.3e-74;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLTFCFLQVLAVHSQGLSAGNNSSTEMEVVFNVEVGRSYCRPMKLVYIADE 60

```

Db	1	MLAMKLETCFLQVLAVHSQGLSAGNNSSTEMEVVFPFNEVWGRCRPMKLVYIADE	60
QY	61	HPNEVSHIFSPSCVLLSRCSCCGDEGLHCVALKTANITWQILKIPNRPDPSHYVENTFS	120
Db	61	HPNEVSHIFSPSCVLLSRCSCCGDEGLHCVALKTANITWQILKIPNRPDPSHYVENTFS	120
QY	121	QDVLCECRPILETTKAER	138
Db	121	QDVLCECRPILETTKAER	138

Search completed: September 13, 2004, 09:50:56
Job time : 131 secs

Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2004, 09:48:49 ; Search time 32 Seconds
(without alignments)
254.903 Million cell updates/sec

Title: US-10-071-370A-4

Perfect score: 846

Sequence: 1 MLAMKLTCTFLQVLAVLH.....RKTGKRKQSKTPTQTEPHL 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:**
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	846	100.0	158	3	US-08-586-039B-39
2	846	100.0	158	4	US-09-699-769-39
3	740	87.5	138	3	US-08-586-039B-37
4	740	87.5	138	4	US-09-699-769-37
5	501.5	59.3	170	2	US-08-039-297B-8
6	501.5	59.3	170	3	US-08-586-039B-45
7	501.5	59.3	170	4	US-09-699-769-45
8	499.5	59.0	170	4	US-09-431-888-5
9	498.5	58.9	154	3	US-08-586-039B-41
10	498.5	58.9	154	4	US-09-699-769-41
11	474.5	56.1	149	1	US-08-469-427A-14
12	474.5	56.1	149	2	US-08-039-297B-2
13	474.5	56.1	149	2	US-08-569-063C-21
14	474.5	56.1	149	3	US-08-795-430-55
15	474.5	56.1	149	3	US-08-586-039B-47
16	474.5	56.1	149	4	US-09-355-700-55
17	474.5	56.1	149	4	US-08-706-054A-5
18	474.5	56.1	149	4	US-09-699-769-47
19	474.5	56.1	149	4	US-09-313-299-5
20	474.5	56.1	149	4	US-08-671-573B-54
21	319.5	37.8	214	3	US-08-586-039B-35
22	319.5	37.8	214	4	US-09-699-769-35
23	316	37.4	214	6	5240848-11
24	315	37.2	188	4	US-09-244-583-28
25	315	37.2	213	4	US-09-574-708A-8
26	315	37.2	215	3	US-08-586-039B-49
27	315	37.2	215	4	US-09-699-769-49

28	315	37.2	215	4	US-09-392-931-8	Sequence 8, Appli
29	315	37.2	215	6	5240848-7	Patent No. 5240848
30	315	37.2	232	2	US-08-999-811-7	Sequence 7, Appli
31	315	37.2	232	2	US-08-824-996-9	Sequence 9, Appli
32	315	37.2	232	3	US-09-042-105-7	Sequence 7, Appli
33	315	37.2	232	4	US-09-574-708A-10	Sequence 10, Appli
34	315	37.2	232	4	US-08-465-968-5	Sequence 5, Appli
35	314.5	37.2	231	5	PCT-US96-09001-10	Sequence 10, Appli
36	313.5	37.1	138	3	US-09-037-983C-16	Sequence 16, Appli
37	313.5	37.1	135	3	US-08-807-992B-3	Sequence 3, Appli
38	313.5	37.1	232	3	US-08-807-992B-4	Sequence 4, Appli
39	312.5	36.9	137	4	US-09-037-983C-17	Sequence 17, Appli
40	312.5	36.9	145	3	US-08-784-551C-2	Sequence 2, Appli
41	312.5	36.9	145	4	US-09-392-932-2	Sequence 4, Appli
42	312.5	36.9	145	4	US-09-574-708A-4	Sequence 2, Appli
43	312.5	36.9	145	4	US-09-037-983C-2	Sequence 2, Appli
44	312.5	36.9	145	4	US-09-428-909A-2	Sequence 4, Appli
45	312.5	36.9	145	4	US-09-392-931-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-586-039B-39
; Sequence 39, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-586-039B-39

Query Match 100.0%; Score 846; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.5e-91;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	Query Match	100.0%	Score 846;	DB 4;	Length 158;
	Best Local Similarity	100.0%;	Pred. NO. 6.5e-91;		
	Matches 158;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	MLAKLFTCTQLVLAGLAVHSGALSGAGNSTEMEVVPFNEVWGRSYCRPMEKLVYIADE	60		
Db	1	MLAKLFTCTQLVLAGLAVHSGALSGAGNSTEMEVVPFNEVWGRSYCRPMEKLVYIADE	60		
OV	61	HENEVSHIFPSRCVLLSRCSGGCDGELHCVALKXTANITMOILKIPNDRDPHSYVMTFS	120		

```

Db      61  HPNEVSHIFSPCVLLSRCSGCCGDEGLHCVALKTANITMQILKTPPNRDPHSYVEMTFS 120
QY      121  QDVLCRCRPILETTKAERRKTKGKRKQSKTPTQTEEPHL 158
Db      121  QDVLCRCRPILETTKAERRKTKGKRKQSKTPTQTEEPHL 158

RESULT 3
US-08-586-039B-37
; Sequence 37, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-586-039B-37

Query Match      87.5%; Score 740; DB 3; Length 138;
Best Local similarity 100.0%; Pred. No. 1.3e-78;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLAMKLFCTCFLQVLAGLAVHVSOGALSAGNNSTEMEVPFNEVWGRSYCRPMKLVYIADE 60
Db      1  MLAMKLFCTCFLQVLAGLAVHVSOGALSAGNNSTEMEVPFNEVWGRSYCRPMKLVYIADE 60
QY      61  HPNEVSHIFSPCVLLSRCSGCCGDEGLHCVALKTANITMQILKTPPNRDPHSYVEMTFS 120
Db      61  HPNEVSHIFSPCVLLSRCSGCCGDEGLHCVALKTANITMQILKTPPNRDPHSYVEMTFS 120
QY      121  QDVLCRCRPILETTKAER 138
Db      121  QDVLCRCRPILETTKAER 138

RESULT 4

```



```
US-09-699-769-37
; Sequence 37, Application US/09699769
; Patent No. 6569434
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
; C SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/699,769
; FILING DATE: 30-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/586,039
; FILING DATE: 16-JAN-1996
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732) 594-3905
; TELEFAX: (732) 594-4720
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-699-769-37
Query Match 87.5%; Score 740; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.3e-78;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLAMKLFCTFLQVLAVHSGQALSAGNSTEMEVVFPFNEVWGRSYCRPMKLVYIADE 60
Db 1 MLAMKLFCTFLQVLAVHSGQALSAGNSTEMEVVFPFNEVWGRSYCRPMKLVYIADE 60
Qy 61 HPNEVSHIFSPCVLLSRSCGCCGDEGLHCVALKTANITMQLKIPNRPDPSYVEMTF 120
Db 61 HPNEVSHIFSPCVLLSRSCGCCGDEGLHCVALKTANITMQLKIPNRPDPSYVEMTF 120
Qy 121 QDVLCECRPILETTKAER 138
Db 121 QDVLCECRPILETTKAER 138
RESULT 5
; Sequence 8, Application US/08039297B
; Patent No. 5919899
; GENERAL INFORMATION:
; APPLICANT: PERSICO, MARIA
; APPLICANT: MAGIONE, DOMENICO
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR A
; TITLE OF INVENTION: HUMAN
; TITLE OF INVENTION: PROTEIN WITH ANGIOGENESIS REGULATIVE PROPERTIES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BEVERIDGE, DeGRANDI, WEILLACHER & YOUNG,
; ADDRESSEE: L.L.P.
; STREET: 1850 M Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/039,297B
; FILING DATE: 19-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT 48315-A90\
; FILING DATE: 27-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weillacher, Robert G
; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 48573
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-659-2811
; TELEFAX: 202-659-1462
; TELEX: WUI64470
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-08-039-297B-8
Query Match 59.3%; Score 501.5; DB 2; Length 170;
Best Local Similarity 61.5%; Pred. No. 1.2e-50;
Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;
Qy 1 MLAMKLFCTFLQVLAVHSGQALSAGNSTEMEVVFPFNEVWGRSYCRPMKLVY 56
Db 1 MPVWMLFPFCFLQVLAVHSGQALSAGNSTEMEVVFPFNEVWGRSYCRALRLVD 60
Qy 57 IADHPNEVSHIFSPCVLLSRSCGCCGDEGLHCVALKTANITMQLKIPNRPDPSYVE 116
Db 61 VVSEYPSVEVHMFSPCVLLSRCTGCGDENLHCVPVETANVTMQLKIRSGDRP-SYVE 119
Qy 117 MTESQDVLCECRPILETTKAERRTKGRKOSKTPQ 152
Db 120 LTFQVRCRCPUREKPKPERRRPGKGRREKQ 155
RESULT 6
US-08-586-039B-45
; Sequence 45, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
```

ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,039B
FILING DATE: 16-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/124,259
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-586-039B-45

Query Match 59.3%; Score 501.5; DB 3; Length 170;
Best Local Similarity 61.5%; Pred. No. 1.2e-50;
Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLOVLGLAVHS-----QGALSAGNNSTEMEVPNEVWGRSYCRPMKLVY 56
DB 1 MPVMLRFPFCQLLQGLALPAVPPQWALSAGNSSEVEVPFQEWGSRYSICALRLVD 60
QY 57 IADHPNEVSHIFSPSCVLLSRCSGCGDEGLHCVALKTANTITMQLKTPPNRDPHSYVE 116
DB 61 VVSEYFSEVHEMFSPSCVLLRCTGCCGDNHLCVPETANVTMQLKIRSGDRP-SYVE 119
QY 117 MTFSDVLCCEPILFTTKAERRKTKGKQSKTPQ 152
DB 120 LTFQHVRCCEPLREKMKPERRPKRGKRRREKQ 155

RESULT 7
US-09-699-769-45
Sequence 45, Application US/09699769
Patent No. 6569434
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
Thomas Jr., Kenneth A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/699,769
FILING DATE: 30-Oct-2000

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/586,039
FILING DATE: 16-JAN-1996
APPLICATION NUMBER: 08/124,259
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-3905
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-699-769-45

Query Match 59.3%; Score 501.5; DB 4; Length 170;
Best Local Similarity 61.5%; Pred. No. 1.2e-50;
Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLOVLGLAVHS-----QGALSAGNNSTEMEVPNEVWGRSYCRPMKLVY 56
DB 1 MPVMLRFPFCQLLQGLALPAVPPQWALSAGNSSEVEVPFQEWGSRYSICALRLVD 60
QY 57 IADHPNEVSHIFSPSCVLLSRCSGCGDEGLHCVALKTANTITMQLKTPPNRDPHSYVE 116
DB 61 VVSEYFSEVHEMFSPSCVLLRCTGCCGDNHLCVPETANVTMQLKIRSGDRP-SYVE 119
QY 117 MTFSDVLCCEPILFTTKAERRKTKGKQSKTPQ 152
DB 120 LTFQHVRCCEPLREKMKPERRPKRGKRRREKQ 155

RESULT 8
US-09-431-888-5
Sequence 5, Application US/09431888A
Patent No. 6541008
GENERAL INFORMATION:
APPLICANT: Wise, Lyn M
APPLICANT: Mercer, Andrew A
APPLICANT: Savory, Loreen J
APPLICANT: Fleming, Stephen B
APPLICANT: Stacker, Stephen
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
FILE REFERENCE: Sequence Listing for 09/431,833
Patent No. 6541008
CURRENT APPLICATION NUMBER: US/09/431,888A
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 60/106,689
EARLIER FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/106,800
EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-431-888-5

Query Match 59.0%; Score 499.5; DB 4; Length 170;
Best Local Similarity 61.5%; Pred. No. 2e-50;

Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

QY 1 MLAMKLFCTFLOVLAVHS-----QGLSAGNNSTEMEVVFNWGRSYCRPMKLVY 56
Db 1 MPVMRLFFCFLOQLAGLALPAVPPQWALSAGNSSEVEVFPQWGRSYCRALERLVD 60

QY 57 IADEHPNEVSHIFSPSCVLLSRGCGGDEGLHCVALKTANITMQLIKIPNRPDPSHYVE 116
Db 61 VVSEYPSVEHMFSPSCVLLSRCTGCGGDEGLHCVETANTVMQLIKIRSGDRP-SYVE 119

QY 117 MTFSDVLCRPILETTKAERRKTKGKRKQSKTPQ 152
Db 120 LTFSDVLCRPILETTKAERRKTKGKRKRRREQ 155

RESULT 9
US-08-586-039B-41
; Sequence 41, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: US-08-586-039B-41

Query Match 58.9%; Score 498.5; DB 3; Length 154;
Best Local Similarity 62.1%; Pred. No. 2.3e-50;
Matches 95; Conservative 23; Mismatches 30; Indels 5; Gaps 2;

QY 1 MLAMKLFCTFLOVLAVHS-----QGLSAGNNSTEMEVVFNWGRSYCRPMKLVY 56
Db 1 MPVMRLFFCFLOQLAGLALPAVPPQWALSAGNSSEVEVFPQWGRSYCRALERLVD 60

QY 57 IADEHPNEVSHIFSPSCVLLSRGCGGDEGLHCVALKTANITMQLIKIPNRPDPSHYVE 116
Db 61 VVSEYPSVEHMFSPSCVLLSRCTGCGGDEGLHCVETANTVMQLIKIRSGDRP-SYVE 119

QY 117 MTFSDVLCRPILETTKAERRKTKGKRKQSK 149
Db 120 LTFSDVLCRPILETTKAERRKTKGKRKRR 152

RESULT 10
US-09-699-769-41
; Sequence 41, Application US/09699769
; Patent No. 6569434
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
; C SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/699,769
; FILING DATE: 30-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/586,039
; FILING DATE: 16-JAN-1996
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732) 594-3905
; TELEFAX: (732) 594-4720
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-699-769-41

Query Match 58.9%; Score 498.5; DB 4; Length 154;
Best Local Similarity 62.1%; Pred. No. 2.3e-50;
Matches 95; Conservative 23; Mismatches 30; Indels 5; Gaps 2;

QY 1 MLAMKLFCTFLOVLAVHS-----QGLSAGNNSTEMEVVFNWGRSYCRPMKLVY 56
Db 1 MPVMRLFFCFLOQLAGLALPAVPPQWALSAGNSSEVEVFPQWGRSYCRALERLVD 60

QY 57 IADEHPNEVSHIFSPSCVLLSRGCGGDEGLHCVALKTANITMQLIKIPNRPDPSHYVE 116
Db 61 VVSEYPSVEHMFSPSCVLLSRCTGCGGDEGLHCVETANTVMQLIKIRSGDRP-SYVE 119

117 MTFSDVLCRPILETTKAERRKTKGKRKQSK 149
120 LTFSDVLCRPILETTKAERRKTKGKRKRR 152

RESULT 11

US-08-469-427A-14
; Sequence 14, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Alitalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979cp2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-427A-14

Query Match 56.1%; Score 474.5; DB 1; Length 149;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

QY 1 MLAMKLTCTFLQVLAVHS----QGALSAGNNSTEMEVPPNEVWGRSYCRPMKLVY 56
Db 1 MPVMRLFPCLQLLAGLALPVPVPPQWALSAGNSSEVEVPFQEVWGRSYCRALERLVD 60
QY 57 IADENHNEVSHIFSPSCVLLSRCSGCCGDEGLHCVALKTANITMQLKIPPNRDPHSYVE 116
Db 61 VVSETPSEVHEMFSPSCVLSLLRCTGCCGDNHLCVPVETANVTMQLLKIRSGDRP-SYVE 119
QY 117 MTFSDVLCRCRPILETTKAER 138
Db 120 LTFSSHVRCECRPLREKMKPER 141

RESULT 12

US-08-039-297B-2
; Sequence 2, Application US/08039297B
; Patent No. 5919899
; GENERAL INFORMATION:
; APPLICANT: PERSICO, MARIA
; APPLICANT: MAGNONE, DOMENICO
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR A
; TITLE OF INVENTION: HUMAN
; TITLE OF INVENTION: PROTEIN WITH ANGIOGENESIS REGULATIVE PROPERTIES

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BEVERIDGE, DeGRANDI, WEILLACHER & YOUNG,
; ADDRESSEE: L.L.P.
; STREET: 1850 M Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/039,297B
; FILING DATE: 19-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT 48315-A90\
; FILING DATE: 27-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weillacher, Robert G
; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 48573
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-659-2811
; TELEFAX: 202-659-1462
; TELEX: WUI64470
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-08-039-297B-2

Query Match 56.1%; Score 474.5; DB 2; Length 149;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;
QY 1 MLAMKLTCTFLQVLAVHS----QGALSAGNNSTEMEVPPNEVWGRSYCRPMKLVY 56
Db 1 MPVMRLFPCLQLLAGLALPVPVPPQWALSAGNSSEVEVPFQEVWGRSYCRALERLVD 60
QY 57 IADENHNEVSHIFSPSCVLLSRCSGCCGDEGLHCVALKTANITMQLKIPPNRDPHSYVE 116
Db 61 VVSETPSEVHEMFSPSCVLSLLRCTGCCGDNHLCVPVETANVTMQLLKIRSGDRP-SYVE 119
QY 117 MTFSDVLCRCRPILETTKAER 138
Db 120 LTFSSHVRCECRPLREKMKPER 141

RESULT 13

US-08-569-063C-21
; Sequence 21, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8840
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-063C-21

Query Match 56.1%; Score 474.5; DB 2; Length 149;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLAMKLTFCLOVLAVHS-----QGLSAGNNSTEMEVVFNWGRSYCRPMKLVY 56
Db 1 MPVNRLEPFCLOLQAGLALPAVPPQWALSAGNSSEVVPFQVWGRSYCRALERLVD 60

Qy 57 IADHPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTNITMQLKIPNRPDPSYVE 116
Db 61 VVSEYSEVHEMFSPSCVLLRCTGCGDENLHCVPVETANVTMQLKIRSGDRP-SYVE 119

Qy 117 MTFSDVLCRCRPILETTKAER 138
Db 120 LTFQSHVRCRPLREXMKPER 141

RESULT 14
US-08-795-430-55
Sequence 55, Application US/08795430
Patent No. 6130071
GENERAL INFORMATION:
APPLICANT: Aitalco, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-430-55

Query Match 56.1%; Score 474.5; DB 3; Length 149;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLAMKLTFCLOVLAVHS-----QGLSAGNNSTEMEVVFNWGRSYCRPMKLVY 56
Db 1 MPVNRLEPFCLOLQAGLALPAVPPQWALSAGNSSEVVPFQVWGRSYCRALERLVD 60

Qy 57 IADHPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTNITMQLKIPNRPDPSYVE 116
Db 61 VVSEYSEVHEMFSPSCVLLRCTGCGDENLHCVPVETANVTMQLKIRSGDRP-SYVE 119

Qy 117 MTFSDVLCRCRPILETTKAER 138
Db 120 LTFQSHVRCRPLREXMKPER 141

RESULT 15
US-08-586-039B-47
Sequence 47, Application US/08586039B
Patent No. 6140073
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
APPLICANT: Thomas Jr, Kenneth A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
TITLE OF INVENTION: SUBUNIT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-586-039B-47

Query Match          56.1%; Score 474.5; DB 3; Length 149;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

QY 1 MLAMKLTCTFLQVLGLAVHS----QCALSGNNSTEMEVVPPFNEVWGRSYCRPMKLVY 56
Db 1 MPVMEFLPCFLQLLAGLALFAVPPQQWALSAGNSSEVVPFQEVWGRSYCRALERLVD 60

QY 57 IADEHNEVSHIFSPSCVLLSRCCGCGDBGLHCVALKTANITMOILKIPPNRDPHSYVE 116
Db 61 VVSEYFSEVHFSPSCVSLLRCTGCCGDNLHCVPETANVTMQLLKIRSGDRP-SYVE 119

QY 117 MTFSDVLCECRPILETTKAER 138
Db 120 LTFSDVHRCRCRPLREKMKPER 141

```

Search completed: September 13, 2004, 09:54:49
Job time : 33 secs

1 MIAMKLIPTCFLOVLAVHSQALSAGNNSTEMEVPFNEVWGRSYCRPMEKLVYIADE 60


```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-439-337A-9

Query Match      59.0%; Score 499.5; DB 12; Length 170;
Best Local Similarity 61.5%; Pred. No. 5.6e-46;
Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLQVLAVHS-----QGALSAGNNSTEMEVVFNWGRSYCRPMKLVY 56
DB 1 MPVWRLFPFCFLQVLAVHS-----QGALSAGNNSTEMEVVFNWGRSYCRALERLVD 60

QY 57 IADHPNEVSHIFSPSCVLLSRGCGGDEGLHCVALKTANITMQLKIPNRPDPSYVE 116
DB 61 VVSEYSEVEHMFSPSCVLLSRCTGCGGDEDLHCVPTETANVTMQLKIRSGDRP-SYVE 119

QY 117 MTFSDVLCRCRPILETTKAERKTKGKRKSKTPQ 152
DB 120 LTFQSHVRCRCRPLREKMKPERRRPKGRKRRNQ 155

RESULT 5
US-10-303-997B-9
; Sequence 9, Application US/10303997B
; Publication No. US20030211994A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-303-997B-9

Query Match      59.0%; Score 499.5; DB 12; Length 170;
Best Local Similarity 61.5%; Pred. No. 5.6e-46;
Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLQVLAVHS-----QGALSAGNNSTEMEVVFNWGRSYCRPMKLVY 56
DB 1 MPVWRLFPFCFLQVLAVHS-----QGALSAGNNSTEMEVVFNWGRSYCRALERLVD 60

QY 57 IADHPNEVSHIFSPSCVLLSRGCGGDEGLHCVALKTANITMQLKIPNRPDPSYVE 116
DB 61 VVSEYSEVEHMFSPSCVLLSRCTGCGGDEDLHCVPTETANVTMQLKIRSGDRP-SYVE 119

QY 117 MTFSDVLCRCRPILETTKAERKTKGKRKSKTPQ 152
DB 120 LTFQSHVRCRCRPLREKMKPERRRPKGRKRRNQ 155
```

```

RESULT 6
US-10-352-153--5
; Sequence 5, Application US/10352153
; Publication No. US20030211101A1
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Lasting for 09/431,833
; CURRENT APPLICATION NUMBER: US/10/352,153
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US/09/431,888A
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,689
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,800
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-352-153-5

Query Match      59.0%; Score 499.5; DB 12; Length 170;
Best Local Similarity 61.5%; Pred. No. 5.6e-46;
Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLQVLAVHS-----QGALSAGNNSTEMEVVFNWGRSYCRPMKLVY 56
DB 1 MPVWRLFPFCFLQVLAVHS-----QGALSAGNNSTEMEVVFNWGRSYCRALERLVD 60

QY 57 IADHPNEVSHIFSPSCVLLSRGCGGDEGLHCVALKTANITMQLKIPNRPDPSYVE 116
DB 61 VVSEYSEVEHMFSPSCVLLSRCTGCGGDEDLHCVPTETANVTMQLKIRSGDRP-SYVE 119

QY 117 MTFSDVLCRCRPILETTKAERKTKGKRKSKTPQ 152
DB 120 LTFQSHVRCRCRPLREKMKPERRRPKGRKRRNQ 155

RESULT 7
US-10-131-600-9
; Sequence 9, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Karl
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
```

RESULT 9
US-10-211-462-115
; Sequence 115, Application US/10211462

Fri Sep 17 12:13:00 2004

```
; PRIOR APPLICATION NUMBER: 08/510,133
; PRIOR FILING DATE: 1995-08-01
; PRIOR APPLICATION NUMBER: 08/340,011
; PRIOR FILING DATE: 1994-11-14
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 55
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human PIGF
US-10-201-386-55

Query Match          56.1%; Score 474.5; DB 14; Length 149;
Best Local Similarity 64.1%; Pred. No. 2.5e-43;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLOVLAVHS-----QGALSAGNNSTEMEVVPPFQVWGRSYCRPMKLVY 56
Db 1 MPVMRLFPFCFLQQLAGLALPAVPPQQWALSAGNSSEVEVPPFQVWGRSYCRALERLVD 60

QY 57 IADHPNEVSHIFSPCVLLSRSCGCGDEGLHCVALKTNITWQILKIPNDRDPHSYVE 116
Db 61 VVSEYSPSEVHEMFSPSCVSLRCTGCCGDNELHCVPTANVTMQLKIRSGDRP-SYVE 119

QY 117 MTFSDVLCRCPLETTKAER 138
Db 120 LTFSQHVRCECRPLREKMKPER 141

RESULT 11
US-10-262-538-28
; Sequence 28, Application US/10262538
; Publication No. US20030113324A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: NEUROPININ/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCE: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 28
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-538-28

Query Match          56.1%; Score 474.5; DB 14; Length 149;
Best Local Similarity 64.1%; Pred. No. 2.5e-43;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLOVLAVHS-----QGALSAGNNSTEMEVVPPFQVWGRSYCRPMKLVY 56
Db 1 MPVMRLFPFCFLQQLAGLALPAVPPQQWALSAGNSSEVEVPPFQVWGRSYCRALERLVD 60

QY 57 IADHPNEVSHIFSPCVLLSRSCGCGDEGLHCVALKTNITWQILKIPNDRDPHSYVE 116
Db 61 VVSEYSPSEVHEMFSPSCVSLRCTGCCGDNELHCVPTANVTMQLKIRSGDRP-SYVE 119

QY 117 MTFSDVLCRCPLETTKAER 138
Db 120 LTFSQHVRCECRPLREKMKPER 141

RESULT 12
US-10-021-660-102
; Sequence 102, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynnne, Richard

; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-102

Query Match          56.1%; Score 474.5; DB 14; Length 149;
Best Local Similarity 64.1%; Pred. No. 2.5e-43;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLOVLAVHS-----QGALSAGNNSTEMEVVPPFQVWGRSYCRPMKLVY 56
Db 1 MPVMRLFPFCFLQQLAGLALPAVPPQQWALSAGNSSEVEVPPFQVWGRSYCRALERLVD 60

QY 57 IADHPNEVSHIFSPCVLLSRSCGCGDEGLHCVALKTNITWQILKIPNDRDPHSYVE 116
Db 61 VVSEYSPSEVHEMFSPSCVSLRCTGCCGDNELHCVPTANVTMQLKIRSGDRP-SYVE 119

QY 117 MTFSDVLCRCPLETTKAER 138
Db 120 LTFSQHVRCECRPLREKMKPER 141

RESULT 13
US-10-346-802-5
; Sequence 5, Application US/10346802
; Publication No. US20030166873A1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; TITLE OF INVENTION: VEGF-RELATED PROTEIN
; FILE REFERENCE: P0963R1D1
; CURRENT APPLICATION NUMBER: US/10/346,802
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US/09/313,299B
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/706,054
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/003,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-09-08
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Human
; LOCATION: 1-149
; OTHER INFORMATION: Sequence source: PIGF-131
US-10-346-802-5

Query Match          56.1%; Score 474.5; DB 14; Length 149;
Best Local Similarity 64.1%; Pred. No. 2.5e-43;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

QY 1 MLAMKLTFCFLOVLAVHS-----QGALSAGNNSTEMEVVPPFQVWGRSYCRPMKLVY 56
Db 1 MPVMRLFPFCFLQQLAGLALPAVPPQQWALSAGNSSEVEVPPFQVWGRSYCRALERLVD 60
```

```

; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatenIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-128

```

```

RESULT 14
US-10-116-275-226
; Sequence 226, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04

```

Search completed: September 13, 2004, 10:05:10
Job time : 128 secs

Query Match	56.1%	Score 474.5	DB 15	Length 149
Best Local Similarity	64.1%	Pred. No. 2.5e-43		
Matches	91	Conservative 19	Mismatches 27	Indels 5
Gaps	2			
QY	1	MLAMKLFTECLOVLAGLAVHS----	QALSAAGNNSTEME	VVPFNEVGRSYCRMEKLY 56
Db	1	MPVNRFPFCQLLAGLALPAVP	QQWALSAGNSSE	VVPFQEVGRSYCRALERIVD 60
QY	57	IADHEHNEVSHIESPCVLLSRCS	CGCGDLCHVALKTANIT	MQILKIPNRRDPHSVE 116
Db	61	VVSEYSEVHEHESPVS	VLRTGTCGCDENLHCVP	VTANVTMQLLKIRSGDRP -SYVE 119
QY	117	MTFSQDVLCECRPILET	TKAER 138	
Db	120	LTFOSHVRCRPLREK	KPER 141	

US-10-440-464-128
; Sequence 128, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874

1 / TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
2 /
3 / TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
4 /
5 / FILE REFERENCE: 038602/1592
6 /
7 / CURRENT APPLICATION NUMBER: US/10/440,464
8 /
9 / CURRENT FILING DATE: 2003-05-19
10 /
11 / PRIOR APPLICATION NUMBER: 60/380,872
12 /
13 / PRIOR FILING DATE: 2002-05-17
14 /
15 / PRIOR APPLICATION NUMBER: 60/448,922
16 /
17 / PRIOR FILING DATE: 2003-02-24
18 /
19 / PRIOR APPLICATION NUMBER: 60/448,874
20 /

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2004, 09:34:08 ; Search time 23 Seconds
(without alignments)
357.699 Million cell updates/sec

Title: US-10-071-370A-4

Perfect score: 846

Sequence: 1 MLAMKLFCTFLQVLGLAVH.....RKTGKRKOSKTPQTEPHL 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	100.0	158	1	PLGF_RAT
2	785	92.8	158	1	PLGF_MOUSE
3	450.5	53.3	221	1	PLGF_HUMAN
4	426.5	50.4	149	1	PLGF_BOVIN
5	322.5	38.1	214	1	VEGA_CANFA
6	320.5	37.9	214	1	VEGA_MOUSE
7	319.5	37.8	214	1	VEGA_RAT
8	315	37.2	232	1	VEGA_HUMAN
9	296.5	35.0	190	1	VEGA_PIG
10	294.5	34.8	190	1	VEGA_HORSE
11	291.5	34.5	216	1	VEGA_CHICK
12	283.5	33.5	190	1	VEGA_BOVIN
13	282.5	33.4	190	1	VEGA_MESAU
14	282	33.3	146	1	VEGA_SHEEP
15	280.5	33.2	164	1	VEGA_CAVPO
16	189	22.3	133	1	VEGH_ORFN2
17	188	22.2	207	1	VEGB_MOUSE
18	182	21.5	207	1	VEGB_HUMAN
19	179.5	21.2	207	1	VEGB_BOVIN
20	179	21.2	135	1	VEGB_RAT
21	174	20.6	358	1	VEGD_MOUSE
22	167	19.7	148	1	VEGH_ORFN7
23	158	18.7	354	1	VEGD_HUMAN
24	153	18.1	326	1	VEGD_RAT
25	144	17.0	419	1	VEGC_HUMAN
26	140	16.5	415	1	VEGC_MOUSE
27	114	13.5	225	1	PDGB_RAT
28	112	13.2	241	1	PDGB_MOUSE
29	110	13.0	245	1	PDGB_FELCA
30	108	12.8	241	1	PDGB_HUMAN
31	105.5	12.5	241	1	PDGB_SHEEP
32	99.5	11.8	213	1	PDGA_RABIT
33	96.5	11.4	226	1	TSIS_SMSAV

RESULT 1
PLGF_RAT ID PLGF_RAT STANDARD; PRET; 158 AA.

AC Q63434; 211 1 PDGA_MOUSE

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Placenta growth factor precursor (PLGF).

GN PLGF.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

[1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=95221439; PubMed=7706320;

RA Disalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,

RA Soderman D.D., Palisi T.M., Sullivan K.A., Thomas K.A.;

RT "Purification and characterization of a naturally occurring vascular

RL J. Biol. Chem. 270:7717-7723(1995).

CC -I- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth, stimulating their proliferation and migration. It binds to receptor VEGFR-1/Flt1 (By similarity).

CC -I- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as heterodimer with VEGF/VEGF-A.

CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -I- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; L40030; AAA97426.1; --

DR PIR; A56125; A56125.

DR HSSP; P49763; 1FZV.

DR InterPro; IPR000072; PD_growth_factor.

DR Fram; PF00341; PDGF; 1.

DR PRODOM; PD001629; PD_growth_factor; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS00278; PDGF_2; 1.

KW Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal.

FT SIGNAL 1 23 OR 26.

FT CHAIN 24 158 PLACENTA GROWTH FACTOR.

FT DISULFID 48 90 BY SIMILARITY.

FT DISULFID 79 125 BY SIMILARITY.

FT DISULFID 83 127 BY SIMILARITY.

FT DISULFID 73 73 INTERCHAIN (BY SIMILARITY).

FT DISULFID 82 82 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 29 29 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 30 30 N-LINKED (GLCNAC...).

ALIGNMENTS

P20033 mus musculus
P28576 rattus norv
P04085 homo sapien
O35757 rattus norv
P13698 xenopus lae
Q8wx14 homo sapien
Q9pkx2 chlamydia m
P30970 acanthopagr
P06607 drosophila
Q8vib2 rattus norv
P19951 sea mays (m
P46295 chlamydomon

34 94.5 11.2 211 1 PDGA_MOUSE
35 92.5 10.9 204 1 PDGA_RAT
36 89.5 10.6 211 1 PDGA_HUMAN
37 88.5 10.5 126 1 VEGC_RAT
38 83 9.8 226 1 PDGA_XENLA
39 81 9.6 607 1 THEA_HUMAN
40 77.5 9.2 326 1 Y338_CHLMU
41 77 9.1 117 1 GLHA_ACALA
42 77 9.1 420 1 VIT3_DROME
43 75 8.9 731 1 DAXX_RAT
44 74.5 8.8 150 1 R142_MAIZE
45 74.5 8.8 153 1 RS14_CHLRE

```

FT CARBOHYD 97 97 N-LINKED (GLCNAC...).
SQ SEQUENCE 158 AA; 17681 MW; B4771373A82E15B9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 846; DB 1; Length 158;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLFTCFLOVLAVHVSQALSGAGNNSTEMEVVPPNEVWGRSYCRPMKLVYIADE 60
Db 1 MLAMKLFTCFLOVLAVHVSQALSGAGNNSTEMEVVPPNEVWGRSYCRPMKLVYIADE 60
QY 61 HENEVSHIFSPSCVLLSRCGCCGDEGLHCVALKTNITMQLKPPNDRPHSYVEMTFS 120
Db 61 HENEVSHIFSPSCVLLSRCGCCGDEGLHCVALKTNITMQLKPPNDRPHSYVEMTFS 120
QY 121 QDVLCRPILETTKAERKTKGKRKQSKTPTQTEPHL 158
Db 121 QDVLCRPILETTKAERKTKGKRKQSKTPTQTEPHL 158

RESULT 2
PLGF MOUSE
ID PLGF MOUSE STANDARD; PRT; 158 AA.
AC P49764;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Placenta growth factor precursor (PLGF).
GN PGF OR PLGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97059399; PubMed=8903720;
RA Dipalma T., Tucci M., Russo G., Maglione D., Lago C.T., Romano A.,
RA Saccone S., della Valle G., de Gregorio L., Dragani T.A.,
RA Viglietto G., Persico M.G.;
RT "The placenta growth factor gene of the mouse.";
RL Mamm. Genome 7:6-12(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=NIH Swiss;
RX MEDLINE=98065381; PubMed=9401819;
RA Achen M.G., Gad J.M., Stacker S.A., Wilks A.P.;
RT "Placenta growth factor and vascular endothelial growth factor are
RT co-expressed during early embryonic development.";
RL Growth Factors 15:69-80(1997).
CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC cell growth, stimulating their proliferation and migration. It
CC binds to receptor VEGFR-1/Flt1 (By similarity).
CC -!- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as
CC heterodimer with VEGF/VEGF-A (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC -----
CC EMBL; X80171; CAAS56453.1;
CC DR EMBL; X36793; CAAS5587.1;
CC DR HSP; P49763; IFLV.
CC DR MGD; MGI:105095; Pgf.
CC DR InterPro; IPR000072; PD_growth_factor.
CC DR Pfam; PF00341; PDGF; 1.
CC DR ProDom; PD001629; PD_growth_factor; 1.

```

```

DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 158 PLACENTA GROWTH FACTOR.
FT DISULFID 48 90 BY SIMILARITY.
FT DISULFID 79 125 BY SIMILARITY.
FT DISULFID 83 127 BY SIMILARITY.
FT DISULFID 73 73 INTERCHAIN (BY SIMILARITY).
FT DISULFID 82 82 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 29 29 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 158 AA; 17876 MW; F16128BEA0790438 CRC64;

Query Match
Best Local Similarity 92.8%; Score 785; DB 1; Length 158;
Matches 145; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLAMKLFTCFLOVLAVHVSQALSGAGNNSTEMEVVPPNEVWGRSYCRPMKLVYIADE 60
Db 1 MLAMKLFTCFLOVLAVHVSQALSGAGNNSTEMEVVPPNEVWGRSYCRPMKLVYILDE 60
QY 61 HENEVSHIFSPSCVLLSRCGCCGDEGLHCVALKTNITMQLKPPNDRPHSYVEMTFS 120
Db 61 YPDEVSHIFSPSCVLLSRCGCCGDEGLHCVPITANITMQLKPPNDRPHSYVEMTFS 120
QY 121 QDVLCRPILETTKAERKTKGKRKQSKTPTQTEPH 157
Db 121 QDVLCRPILETTKAERKTKGKRKRSNSTEPH 157

RESULT 3
PLGF HUMAN
ID PLGF HUMAN STANDARD; PRT; 221 AA.
AC P49763; Q07101; Q9BV78; Q9Y6S8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Placenta growth factor precursor (PLGF).
GN PGF OR PLGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM PLGF-1).
RC TISSUE=Placenta;
RX MEDLINE=92021031; PubMed=1924389;
RA Maglione D., Guerriero V., Viglietto G., Delli-Bovi P., Persico M.G.;
RT "Isolation of a human placenta cDNA coding for a protein related to
RT the vascular permeability factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9267-9271(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM PLGF-2).
RC TISSUE=Placenta;
RX MEDLINE=94198032; PubMed=8148155;
RA Hauser S.D., Weich H.A.;
RT "A heparin-binding form of placenta growth factor (PLGF-2) is
RT expressed in human umbilical vein endothelial cells and in
RT placenta.";
RL Growth Factors 9:259-268(1993).
RN [3]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM PLGF-2).
RX MEDLINE=93205407; PubMed=7681160;
RA Maglione D., Guerriero V., Viglietto G., Ferraro M.G., Aprelikova O.,
RA Alitalo K., del Vecchio S., Lei K.-J., Chou J.-Y., Persico M.G.;
RT "Two alternative mRNAs coding for the angiogenic factor, placenta
RT growth factor (PLGF), are transcribed from a single gene of
RT chromosome 14.";
RL Oncogene 8:925-931(1993).
RN [4]

```

CC	binds to receptor VEGFR-1/Flt1. PlGF-2 binds neuropilin-1 and 2 in a heparin-dependent manner.	
CC	-! SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as heterodimer with VEGF/VEGF-A. PlGF-3 is found both as homodimer and as monomer.	
CC	-! SUBCELLULAR LOCATION: The three forms are secreted but PlGF-2 appears to remain cell attached unless released by heparin.	
CC	-! ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3; Name=PlGF-3;	
CC	IsoId=P49763-1; Sequence=Displayed;	
CC	Name=PlGF-1; Synonyms=PlGF-131;	
CC	IsoId=P49763-2; Sequence=VSP_004644;	
CC	Name=PlGF-2; Synonyms=PlGF-152;	
CC	IsoId=P49763-3; Sequence=VSP_004644, VSP_004645;	
CC	-! TISSUE SPECIFICITY: While the three forms are present in most placental tissues, the PlGF-2 is specific to early (8 week) placenta and only PlGF-1 is found in the colon and mammary carcinomas.	
CC	-! DOMAIN: PlGF-2 contains a basic insert which acts as a cell retention signal.	
CC	-! PTM: N-glycosylated.	
CC	-! SIMILARITY: Belongs to the PDGF/VEGF growth factor family.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-----	
CC	EMBL; X54936; CAA38698.1; -;	
DR	EMBL; S72960; AAB30462.2; -;	
DR	EMBL; S57152; AAB25832.2; ALT_SEQ.	
DR	EMBL; AC006530; AAD30179.1; -;	
DR	EMBL; BC001422; AAH01422.1; -;	
DR	EMBL; BC007789; AAH07789.1; -;	
DR	EMBL; BC007255; AAH07255.1; -;	
DR	EMBL; AJ8411; CAA01393.1; -;	
DR	PIR; A41236; A41236.	
DR	PDB; IFZV; 09-MAY-01.	
DR	Genew; HGNC:8893; PGF.	
DR	MIM; 601121; -;	
DR	GO; GO:0008083; F:growth factor activity; TAS.	
DR	GO; GO:0007267; P:cell-cell signaling; TAS.	
DR	GO; GO:0008284; P:positive regulation of cell proliferation; TAS.	
DR	GO; GO:0007165; P:signal transduction; TAS.	
DR	InterPro; IPR000072; PD_growth_factor.	
DR	Pfam; PF00341; PDGF; 1.	
DR	ProDom; PD001629; PD_growth_factor; 1.	
DR	SMART; SM00141; PDGF; 1.	
DR	PROSITE; PS00249; PDGF_1; 1.	
DR	PROSITE; PS0278; PDGF_2; 1.	
DR	Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal;	
KW	Heparin-binding; Alternative splicing; 3D-structure.	
CC	Signal 1 18	
FT	CHAIN 1 18	
FT	SH 19 221 PLACENTA GROWTH FACTOR.	
FT	DOMAIN 193 213 HEPARIN-BINDING (PROBABLE).	
FT	DISULFID 52 94	
FT	DISULFID 83 128	
FT	DISULFID 87 130	
FT	DISULFID 77 77 INTERCHAIN.	
FT	DISULFID 86 86 INTERCHAIN.	
FT	CARBOHYD 33 33 N-LINKED (GLCNAC..) (POTENTIAL).	
FT	CARBOHYD 101 101 N-LINKED (GLCNAC..) (POTENTIAL).	
FT	VARSPPLIC 132 203 Missing (in isoform PlGF-1 and isoform PlGF-2).	
FT	FTID=VSP_004644.	
FT	VARSPPLIC 213 213 R -> RRRPGKRRRREKQPTDCHL (in isoform PlGF-2).	
FT	FTID=VSP_004645.	
FT	CONFLICT 91 N -> D (IN REF. 2).	

FT STRAND 40 41
 FT HELIX 43 50
 FT STRAND 51 51
 FT STRAND 53 60
 FT TURN 61 61
 FT HELIX 62 64
 FT STRAND 73 74
 FT STRAND 77 84
 FT STRAND 86 86
 FT TURN 90 91
 FT STRAND 92 108
 FT TURN 111 112
 FT STRAND 116 132
 SQ SEQUENCE 221 AA; 24788 MW; D364C6A73C1C6987 CRC64;

Query Match 53.3%; Score 450.5; DB 1; Length 221;
 Best Local Similarity 65.2%; Pred. No. 1.2e-39;
 Matches 86; Conservative 18; Mismatches 23; Indels 5; Gaps 2;

QY 1 MLAMKLTCTFLQVLAVHS----QGLSAGNSTEMEVPFNEVWGRSYCRPMKLYV 56
 Db 1 MPVRLFPCTFLQVLAVPVPQQWALSAGNSSEVWPFQEWGRSYCRALERLDV 60
 QY 57 IADEHPNEVSHFSPSCVLLSCGCCGDEGHCHVAKLTANTMTQILKIPNDRPHSYVE 116
 Db 61 VVSEYSEVHEHMFSPSCVLLSCGCCGDEGHCHVAKLTANTMTQILKIRSGDRP-SYVE 119
 QY 117 MTFSDVLCRCR 128
 Db 120 LTFQHVRCRCR 131

RESULT 4
 PLGF BOVIN STANDARD; PRT; 149 AA.
 AC Q9XS47:
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Placenta growth factor precursor (PLGF).
 GN PGF OR PLGF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;
 RT "Structure and expression of bovine VEGF family.";
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
 CC cell growth, stimulating their proliferation and migration. It
 CC binds to receptor VEGFR-1/Flt1 (By similarity).
 CC -!- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as
 CC heterodimer with VEGF/VEGF-A (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB004272; BAA77684.1; .
 DR HSSP; P49763; 1F2V.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Pfam; PF00341; PDGF; 1.
 DR ProDom; PD001629; PD_growth_factor; 1.

DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS00249; PDGF_1; 1.
 DR PROSITE; PS00278; PDGF_2; 1.
 KW Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 149 PLACENTA GROWTH FACTOR.
 FT DISULFID 52 94 BY SIMILARITY.
 FT DISULFID 83 128 BY SIMILARITY.
 FT DISULFID 87 130 BY SIMILARITY.
 FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 86 86 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 149 AA; 17094 MW; 1F8EE3B8C745EFC0 CRC64;

Query Match 50.4%; Score 426.5; DB 1; Length 149;
 Best Local Similarity 56.3%; Pred. No. 2.4e-37;
 Matches 80; Conservative 25; Mismatches 32; Indels 5; Gaps 2;

QY 1 MLAMKLTCTFLQVLAVHS----HSQGLSAGNSTEMEVPFNEVWGRSYCRPMKLYV 56
 Db 1 MPTVRLFTCTFLQVLAVLPVPTTQWALSAGNSSEVWPFQEWGRSYCRPVERLDV 60
 QY 57 IADEHPNEVSHFSPSCVLLSCGCCGDEGHCHVAKLTANTMTQILKIPNDRPHSYVE 116
 Db 61 IVSEYSEVHEHMFSPSCVLLSCGCCGDEGHCHVAKLTANTMTQILKIRSGDRP-SYVE 119
 QY 117 MTFSDVLCRCRPILETTKAER 138
 Db 120 MSFQHVRCRCRPLEWKQTR 141

RESULT 5
 VEGA CANFA STANDARD; PRT; 214 AA.
 AC Q9MIV3; Q9XSF3; Q9XSF4; Q9XSF5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
 DE permeability factor) (VPF).
 GN VEGF OR VEGFA.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF-188).
 RC MEDLINE=20125516; PubMed=10661874;
 RA Scheidegger P., Weiglhofer W., Suarez S., Kaser-Hotz B., Steiner R.,
 RA Ballmer-Hofer K., Jaussi R.;
 RT "Vascular endothelial growth factor (VEGF) and its receptors in tumor-
 RL bearing dogs.";
 RL Biol. Chem. 380:1449-1454(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS VEGF-188; VEGF-182 AND VEGF-164).
 RC TISSUE=Heart;
 RA Jingjing L., Roque R.S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
 CC endothelial cell growth. It induces endothelial cell
 CC proliferation, promotes cell migration, inhibits apoptosis, and
 CC induces permeabilization of blood vessels. It binds to the
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
 CC heparin (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
 CC with PLGF (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
 CC to the extracellular matrix unless released by heparin (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;


```
CC Name=VEGF-188;
CC IsoId=Q9MYV3-1; Sequence=Displayed;
CC Name=VEGF-182;
CC IsoId=Q9MYV3-2; Sequence=VSP_004617;
CC Name=VEGF-164;
CC IsoId=Q9MYV3-3; Sequence=VSP_004615, VSP_004616;
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ133758; CAB82426.1; -
CC EMBL; AF133250; AAD29684.1; -
CC EMBL; AF133249; AAD29683.1; -
CC EMBL; AF133248; AAD29682.1; -
CC HSSP; P15692; IVGH.
CC InterPro; IPR000072; PD_growth_factor.
CC Pfam; PF00341; PDGF; 1.
CC ProDom; PD001629; PD_growth_factor; 1.
CC SMART; SM00141; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS0278; PDGF_2; 1.
CC Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT SIGNAL 1
FT CHAIN 27 214
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
FT VARSPLIC 140 140
FT VARSPLIC 141 164
FT VARSPLIC 159 164
FT VARSPLIC 143 143
FT CONFLICT 161 161
FT CONFLICT 161 161
FT SEQUENCE 214 AA; 25175 MW; 0AC980A158C44B27 CRC64;
Query Match 38.1%; Score 322.5; DB 1; Length 214;
Best Local Similarity 49.6%; Pred. No. 2.5e-26;
Matches 64; Conservative 18; Mismatches 46; Indels 1; Gaps 1;
QY 21 SQGLSAGNNSTEMEVVPEVNEVGRSYCRPMEXKLVITADEHPNEVSHIFSPSCVLLSRCS 80
Db 24 SQAPWAGGKHKEHVVKFMDVQVRSYCRPIETLVDIFQYDPEIEYIFRSPCVPLMRG 83
QY 81 GCGDEGLCHVALKANTITMQLKIPNRPDPSHYVEMTFSDVLCECRPILETTKARRK 140
Db 84 GCGNDEGLCVPTPEEFNITQIMREIKPHQGH-IGEMSFLOHKSCECRPKKDRARQEKKS 142
QY 141 TKGRKQSK 149
Db 143 IRGKGQK 151
RESULT 6
VEGA MOUSE STANDARD; PRT; 214 AA.
AC Q00731;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
```

```
GN VEGF OR VEGFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORMS VEGF-1; VEGF-2 AND VEGF-3).
RX MEDLINE=92274860; PubMed=1592003;
RA Breier G., Albrecht U., Sterrer S., Risau W.;
RT "Expression of vascular endothelial growth factor during embryonic
RT angiogenesis and endothelial cell differentiation.";
RL Development 114:521-532(1992).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM VEGF-1).
RX MEDLINE=92355593; PubMed=1644816;
RA Clafey K.P., Wilkison W.O., Spiegelman B.M.;
RT "Vascular endothelial growth factor. Regulation by cell
RT differentiation and activated second messenger pathways.";
RL J. Biol. Chem. 267:16317-16322(1992).
RN [3]
RN SEQUENCE OF 1-3 FROM N.A.
RX MEDLINE=96216498; PubMed=8632007;
RA Shima D.T., Kuroki M., Deutsch U., Ng Y., Adamis A.P., D'Amore P.A.;
RT "The mouse gene for vascular endothelial growth factor. Genomic
RT structure, definition of the transcriptional unit, and
RT characterization of transcriptional and post-transcriptional
RT regulatory sequences.";
RL J Biol. Chem. 271:3877-3883(1996).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -1- SUBCELLULAR LOCATION: VEGF-1 and VEGF-2 are secreted while VEGF-3
CC remains cell-surface associated unless released by heparin.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=VEGF-3; Synonyms=VEGF188;
CC IsoId=Q00731-1; Sequence=Displayed;
CC Name=VEGF-1; Synonyms=VEGF164;
CC IsoId=Q00731-2; Sequence=VSP_004626, VSP_004627;
CC Name=VEGF-2; Synonyms=VEGF120;
CC IsoId=Q00731-3; Sequence=VSP_004628;
CC -1- TISSUE SPECIFICITY: In developing embryos, expressed mainly in the
CC choroid plexus, paraventricular neuroepithelium, placenta and
CC kidney glomeruli. Also found in bronchial epithelium, adrenal
CC gland and in seminiferous tubules of testis. High expression of
CC VEGF continues in kidney glomeruli and choroid plexus in adults.
CC -1- DOMAIN: VEGF-3 contains a basic insert which acts as a cell
CC retention signal.
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S37052; AAB22252.1; -
CC EMBL; S38083; AAB22253.1; -
CC EMBL; S38100; AAB22254.1; -
CC EMBL; M95200; AAA40547.1; -
CC EMBL; U41383; -; NOT_ANNOTATED_CDS.
CC PIR; A44881; A44881.
CC PIR; B44881; B44881.
CC HSSP; P15692; VPF.
CC MGI; MGI:103178; Vegfa.
CC InterPro; IPR000072; PD_growth_factor.
DR
```

RP SEQUENCE OF 27-40.

```

FT  VARSPLIC 165 208 /FTID=VSP_004631.
FT  Missing (in isoform VEGF-A144).
FT  /FTID=VSP_004632.
FT  CONFLICT 101 101 V -> A (IN REF. 2: AAF19212).
SQ  SEQUENCE 214 AA; 25239 MW; 60FBB876F5304946 CRC64;

Query Match 37.8%; Score 319.5; DB 1; Length 214;
Best Local Similarity 48.1%; Pred. No. 5.2e-26;
Matches 62; Conservative 20; Mismatches 46; Indels 1; Gaps 1;

QY 21 SOGALSAGNNSTEMEVVFNVEWGRSCRPMEKLVYIADHPNEVSHFSPSCVLLSRCS 80
DB 24 SQAAPTTEGQKAHEVVVFMDVYQVRSYCRPIETLVDIFQBYVDEIEYFEPSCVPLMRCA 83
QY 81 GCCGDEGLHCVALKANTITMQLKIPPNRDPHSVEMTFSDVLCCECRPILETTKARRK 140
DB 84 GCNDEALECVPTSESNVTQIMRIKHQSOH-IGEMSFLQHSCECRPKKDRTPKPKS 142
QY 141 TKGRRKQSK 149
DB 143 VRGKGKGQK 151

RESULT 8
VEGA HUMAN STANDARD; PRT; 232 AA.
AC P15692; O60720; O75875; Q16889; Q96L82; Q96NWS; Q9H1W8; Q9H1W9;
AC Q9UH58; Q9UL23;
DT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
SEQUENCE FROM N.A. (ISOFORMS VEGF189 AND VEGF165).
RP MEDLINE=90069608; PubMed=2479986;
RA Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT "Vascular endothelial growth factor is a secreted angiogenic
RT mitogen.";
RL Science 246:1306-1309(1989).
RN 2
SEQUENCE FROM N.A. (ISOFORM VEGF189), AND PARTIAL SEQUENCE.
RP MEDLINE=90069609; PubMed=2479987;
RA Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
RA Connolly D.T.;
RT "Vascular permeability factor, an endothelial cell mitogen related to
RT PDGF.";
RL Science 246:1309-1312(1989).
RN 3
SEQUENCE FROM N.A. (ISOFORM VEGF189).
RP MEDLINE=91268072; PubMed=1711045;
RA Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
RA Fiddes J.C., Abraham J.A.;
RT "The human gene for vascular endothelial growth factor: Multiple
RT protein forms are encoded through alternative exon splicing.";
RL J. Biol. Chem. 266:11947-11954(1991).
RN 4
SEQUENCE FROM N.A. (ISOFORM VEGF206).
RP MEDLINE=92168017; PubMed=1791831;
RA Honck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;
RT "The vascular endothelial growth factor family: Identification of a
RT fourth molecular species and characterization of alternative splicing
RT of RNA.";
RL Mol. Endocrinol. 5:1806-1814(1991).
RN 5
SEQUENCE FROM N.A. (ISOFORM VEGF165).
RP MEDLINE=92231879; PubMed=1567395;
RA Weindel K., Marne D., Weich H.A.;

```

```

RT "AIDS-associated Kaposi's sarcoma cells in culture express vascular
RT endothelial growth factor.";
RL Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
RN 6
SEQUENCE FROM N.A. (ISOFORM VEGF145).
RX MEDLINE=97207275; PubMed=9054410;
RA Poltorak Z., Cohen T., Sivan R., Kandelis Y., Spira G., Vlodavsky I.,
RA Keshet E., Neufeld G.;
RT "VEGF145, a secreted vascular endothelial growth factor isoform that
RT binds to extracellular matrix.";
RL J. Biol. Chem. 272:7151-7158(1997).
RN 7
SEQUENCE FROM N.A. (ISOFORM VEGF183).
RP TISSUE=Kidney;
RX MEDLINE=99096474; PubMed=9878851;
RA Lei J., Jiang A., Pei D.;
RT "Identification and characterization of a new splicing variant of
RT vascular endothelial growth factor: VEGF183.";
RL Biochim. Biophys. Acta 1443:400-406(1998).
RN 8
SEQUENCE FROM N.A. (ISOFORM VEGF165).
RP TISSUE=Breast;
RX MEDLINE=98119755; PubMed=9450968;
RA Claffey K.P., Shih S.-C., Mullen A., Diennis S., Cusick J.L.,
RA Abrams K.R., Lee S.W., Detmar M.;
RT "Identification of a human VPF/VEGF 3' untranslated region mediating
RT hypoxia-induced mRNA stability.";
RL Mol. Biol. Cell 9:469-481(1998).
RN 9
SEQUENCE FROM N.A. (ISOFORM VEGF165).
RP TISSUE=Hemangioendothelioma;
RX Murata H., Fukushima J., Hattori S., Okuda K., Yanagi H.;
RT "Human cDNA for the vascular endothelial growth factor isoform
RT VEGF165.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN 10
SEQUENCE FROM N.A. (ISOFORM VEGF148).
RP TISSUE=Renal glomerulus;
RX MEDLINE=99394945; PubMed=10464055;
RA Whittle C.J., Gillespie K.M., Harrison R., Mathieson P.W.,
RA Harper S.J.;
RT "Heterogeneous vascular endothelial growth factor (VEGF) isoform mRNA
RT and receptor mRNA expression in human glomeruli, and the
RT identification of VEGF148 mRNA, a novel truncated splice variant.";
RL Clin. Sci. 97:303-312(1999).
RN 11
SEQUENCE FROM N.A. (ISOFORM VEGF121).
RP Sato J.D., Whitney R.G.;
RT "Human cDNA for vascular endothelial growth factor isoform VEGF121.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN 12
SEQUENCE FROM N.A.
RP Williams S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN 13
SEQUENCE FROM N.A. (ISOFORM VEGF165).
RP Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of vascular endothelial growth factor (VEGF) cDNA.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN 14
SEQUENCE FROM N.A. (ISOFORM VEGF165).
RP TISSUE=Heart;
RX Shan Z.X., Yu X.Y., Lin Q.X., Fu Y.H., Zheng M., Tan H.H., Lin S.G.;
RT "Cloning and identification of vascular endothelial growth factor
RT isoform VEGF165.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN 15
SEQUENCE OF 23-232 FROM N.A. (ISOFORM VEGF165).
RP Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN 16
SEQUENCE OF 114-209 FROM N.A. (ISOFORM VEGF183).
RP

```

RC TISSUE-Retina;
RX MEDLINE=99165303; PubMed=10067980;
RA Jingling L., Xue Y., Agarwal N., Roque R.S.;
RT "Human Muller cells express VEGF183, a novel spliced variant of
RT vascular endothelial growth factor.";
RL Invest. Ophthalmol. Vis. Sci. 40:752-759(1999).
RN [17]
RP PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX MEDLINE=90062112; PubMed=2584205;
RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monseil R.,
RA Siegel N., Haymore B.L., Leimgruber R., Feder J.;
RT "Human vascular permeability factor. Isolation from U937 cells.";
RL J. Biol. Chem. 264:20017-20024(1989).
RN [18]
RP SEQUENCE OF 27-41.
RX MEDLINE=93145946; PubMed=7678805;
RA Fiebig B.L., Jaeger B., Schoellmann C., Weindel K., Wiltling J.,
RA Kochs G., Marne D., Hug H., Welch H.A.;
RT "Synthesis and assembly of functionally active human vascular
RT endothelial growth factor homodimers in insect cells.";
RL Eur. J. Biochem. 211:19-26(1993).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX MEDLINE=97352774; PubMed=9207067;
RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA de Vos A.M.;
RT "Vascular endothelial growth factor: crystal structure and functional
RT mapping of the kinase domain receptor binding site.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX MEDLINE=98035455; PubMed=9351807;
RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT "The crystal structure of vascular endothelial growth factor (VEGF)
RT refined to 1.93-A resolution: multiple copy flexibility and receptor
RT binding.";
RL Structure 5:1325-1338(1997).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX MEDLINE=99119204; PubMed=9922142;
RA Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT "Crystal structure of the complex between VEGF and a receptor-blocking
RT peptide.";
RL Biochemistry 37:17765-17772(1998).
RN [22]
RP STRUCTURE BY NMR OF 34-135.
RX MEDLINE=97477915; PubMed=9336848;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "1H, 13C, and 15N backbone assignment and secondary structure of the
RT receptor-binding domain of vascular endothelial growth factor.";
RL Protein Sci. 6:2250-2260(1997).
RN [23]
RP STRUCTURE BY NMR OF 137-215.
RX MEDLINE=98298440; PubMed=9634701;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "Solution structure of the heparin-binding domain of vascular
RT endothelial growth factor.";
RL Structure 6:637-648(1998).
RN [24]
RP FUNCTION.
RX MEDLINE=21320570; PubMed=11427521;
RA Murphy J.F., Fitzgerald D.J.;
RT "Vascular endothelial growth factor induces cyclooxygenase-dependent
RT proliferation of endothelial cells via the VEGF-2 receptor.";
RL PASEB J. 15:1667-1669(2001).
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC

CC heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -!- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.
CC VEGF165 is more basic, has heparin-binding properties and,
CC although a significant proportion remains cell-associated, most is
CC [17]
Query Match 37.2%; Score 315; DB 1; Length 232;
Best Local Similarity 47.7%; Pred. No. 1.7e-25;
Matches 62; Conservative 21; Mismatches 45; Indels 2; Gaps 2;
QY 21 SQQA-LSAGNNSTEMEVFPFNEVWGRSYCRPMKLVYIADEHPNEVSHFSPCVLLSRC 79
DB 24 SQAAPMAEGGQGHHEVWKFMDVYQSYCHPIETLVDIFQEPDEIEYFKSCVPLMRC 83
QY 80 SGCCGDEGLHCVALKTANITMQLKPPNRDPHSYVEMTFSDVLCCECPLETTKAERR 139
DB 84 GGCNDDEGLCYPTESNTMQLMIRKPHQGH-IGEMSFLOHNKCECPKDKRAQEKK 142
QY 140 KTKGKRKQSK 149
DB 143 SVRGKKGQK 152
RESULT 9
VEGA_PIG
ID VEGA_PIG STANDARD; PRT; 190 AA.
AC P49151; Q9GL52;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VFP).
GN VEGF OR VEGFA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95143284; PubMed=7841203;
RA Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
RT "Nucleotide sequence and expression of the porcine vascular
RT endothelial growth factor.";
RL Biochim. Biophys. Acta 1260:235-238(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee T., Cauty J.M.;
RT "PCR cloning of porcine cardiac vascular endothelial growth factor
RT gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin (By
CC similarity).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----

```

DR EMBL; X81380; CAA57143.1; -.
DR EMBL; AF318502; RAG33064.1; -.
DR PIR; S52130; S52130.
DR HSP; P15692; 1VGH.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 82 127 BY SIMILARITY.
FT DISULFID 86 129 BY SIMILARITY.
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT DISULFID 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 102 102 T -> A (IN REF. 2).
FT CONFLICT 102 102
FT SEQUENCE 190 AA; 22368 MW; 04D40B8D7913047F CRC64;

Query Match 35.0%; Score 296.5; DB 1; Length 190;
Best Local Similarity 48.4%; Pred. No. 1.1e-23;
Matches 62; Conservative 17; Mismatches 40; Indels 9; Gaps 2;

QY 21 SQALSAGNNSTMEVVFNEVWGRSVCYRPMKLVIADEHPNEVSHIFSPSCVLLSRCS 80
Db 24 SQAAPMAEGDKHEVVKFMDVYQSRPIETLVDIFQYDPDEIEYIFKPSCVPLMRCG 83
QY 81 GCGDEGLHCVALKTANITQILKIPNRPDHPHSYVEMTFSQDVLCECRPILETTK----- 135
Db 84 GCNDEGLCVPTAEFTNITQIMRIKPHQSQH-IGEMSFLOHKSCECRPKKDKARQENPC 142
QY 136 ---AERRK 140
Db 143 GPCSERRK 150

RESULT 10
VEGA_HORSE
ID VEGA_HORSE STANDARD; PRT; 190 AA.
AC Q9GKR0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Miura N., Miumi K., Kawahara K., Nakashima M., Fukumitsu S., Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.;
RT "Cloning of cDNA and high-level expression of equine vascular endothelial growth factor (VEGF)".
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB053350; BAB20890.1; -.
DR HSP; P15692; 1VGH.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 82 127 BY SIMILARITY.
FT DISULFID 86 129 BY SIMILARITY.
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 190 AA; 22312 MW; 87E9E161439E5F87 CRC64;

Query Match 34.8%; Score 294.5; DB 1; Length 190;
Best Local Similarity 48.4%; Pred. No. 1.1e-23;
Matches 62; Conservative 15; Mismatches 42; Indels 9; Gaps 2;

QY 21 SQALSAGNNSTMEVVFNEVWGRSVCYRPMKLVIADEHPNEVSHIFSPSCVLLSRCS 80
Db 24 SQAAPMAEGDKHEVVKFMDVYQSRPIETLVDIFQYDPDEIEYIFKPSCVPLMRCG 83
QY 81 GCGDEGLHCVALKTANITQILKIPNRPDHPHSYVEMTFSQDVLCECRPILETTK----- 135
Db 84 GCNDEGLCVPTAEFTNITQIMRIKPHQSQH-IGEMSFLOHKSCECRPKKDKARQENPC 142
QY 136 ---AERRK 140
Db 143 GPCSERRK 150

RESULT 11
VEGA_CHICK
ID VEGA_CHICK STANDARD; PRT; 216 AA.
AC P525B2; Q91420;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Gallus gallus (Chicken), and Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE FROM N.A.
RA SPECIES=Chicken; TISSUE=Heart;
RT Takahashi T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

```

```

RA Flamme I., von Reutern M., Drexler H.C., Syed-Ali S., Risau W.;
RT "Overexpression of vascular endothelial growth factor in the avian
RT embryo induces hypervascularization and increased vascular
RT permeability without alterations of embryonic pattern formation.";
RL Dev. Biol. 171:399-414 (1995).
RN [3]
RP SEQUENCE OF 60-187 FROM N.A. (ISOFORMS VEGF-190 AND VEGF-166).
RC SPECIES=C.c.japonica;
RX MEDLINE=95301109; PubMed=7781909;
RA Flamme I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2
RT (flk-1) are expressed during vasculogenesis and vascular
RT differentiation in the quail embryo.";
RL Dev. Biol. 169:699-712 (1995).
RN [3]
RP FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -! SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PLGF (By similarity).
CC -! ALTERNATIVE PRODUCTS:
CC Comment=Alternative splicing; Named isoforms=3;
CC Name=VEGF-190;
CC IsoId=PS2582-1; Sequences=Displayed;
CC Name=VEGF-166;
CC IsoId=PS2582-2; Sequences=VSP 004633, VSP 004634;
CC Note=Has been shown to exist only in quail so far;
CC Name=VEGF-146;
CC IsoId=PS2582-3; Sequences=VSP_004635, VSP_004636;
CC Note=Has been shown to exist only in quail so far;
CC -! TISSUE SPECIFICITY: Abundantly and equally expressed in heart and
CC liver. In kidney glomeruli, brain and yolk sac, VEGF-166 is 5- to
CC 10-times more abundant than VEGF-190.
CC -! DEVELOPMENTAL STAGE: VEGF-166 is expressed early at day 1 and is
CC upregulated during gastrulation. Expression of VEGF-190 is detectable
CC only from day 2.
CC -! DOMAIN: VEGF-190 contains a basic insert which acts as a cell
CC retention signal.
CC -! SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB011078; BAA24925.1; -.
DR EMBL; S79680; AAB35371.1; -.
DR HSSP; P15692; 1VGH.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR PROSITE; PS02079; PDGF_3; 1.
DR PROSITE; PS02078; PDGF_4; 1.
DR PROSITE; PS02079; PDGF_5; 1.
DR PROSITE; PS02078; PDGF_6; 1.
DR PROSITE; PS02079; PDGF_7; 1.
DR PROSITE; PS02078; PDGF_8; 1.
DR PROSITE; PS02079; PDGF_9; 1.
DR PROSITE; PS02078; PDGF_10; 1.
DR PROSITE; PS02079; PDGF_11; 1.
DR PROSITE; PS02078; PDGF_12; 1.
DR PROSITE; PS02079; PDGF_13; 1.
DR PROSITE; PS02078; PDGF_14; 1.
DR PROSITE; PS02079; PDGF_15; 1.
DR PROSITE; PS02078; PDGF_16; 1.
DR PROSITE; PS02079; PDGF_17; 1.
DR PROSITE; PS02078; PDGF_18; 1.
DR PROSITE; PS02079; PDGF_19; 1.
DR PROSITE; PS02078; PDGF_20; 1.
DR PROSITE; PS02079; PDGF_21; 1.
DR PROSITE; PS02078; PDGF_22; 1.
DR PROSITE; PS02079; PDGF_23; 1.
DR PROSITE; PS02078; PDGF_24; 1.
DR PROSITE; PS02079; PDGF_25; 1.
DR PROSITE; PS02078; PDGF_26; 1.
DR PROSITE; PS02079; PDGF_27; 1.
DR PROSITE; PS02078; PDGF_28; 1.
DR PROSITE; PS02079; PDGF_29; 1.
DR PROSITE; PS02078; PDGF_30; 1.
DR PROSITE; PS02079; PDGF_31; 1.
DR PROSITE; PS02078; PDGF_32; 1.
DR PROSITE; PS02079; PDGF_33; 1.
DR PROSITE; PS02078; PDGF_34; 1.
DR PROSITE; PS02079; PDGF_35; 1.
DR PROSITE; PS02078; PDGF_36; 1.
DR PROSITE; PS02079; PDGF_37; 1.
DR PROSITE; PS02078; PDGF_38; 1.
DR PROSITE; PS02079; PDGF_39; 1.
DR PROSITE; PS02078; PDGF_40; 1.
DR PROSITE; PS02079; PDGF_41; 1.
DR PROSITE; PS02078; PDGF_42; 1.
DR PROSITE; PS02079; PDGF_43; 1.
DR PROSITE; PS02078; PDGF_44; 1.
DR PROSITE; PS02079; PDGF_45; 1.
DR PROSITE; PS02078; PDGF_46; 1.
DR PROSITE; PS02079; PDGF_47; 1.
DR PROSITE; PS02078; PDGF_48; 1.
DR PROSITE; PS02079; PDGF_49; 1.
DR PROSITE; PS02078; PDGF_50; 1.
DR PROSITE; PS02079; PDGF_51; 1.
DR PROSITE; PS02078; PDGF_52; 1.
DR PROSITE; PS02079; PDGF_53; 1.
DR PROSITE; PS02078; PDGF_54; 1.
DR PROSITE; PS02079; PDGF_55; 1.
DR PROSITE; PS02078; PDGF_56; 1.
DR PROSITE; PS02079; PDGF_57; 1.
DR PROSITE; PS02078; PDGF_58; 1.
DR PROSITE; PS02079; PDGF_59; 1.
DR PROSITE; PS02078; PDGF_60; 1.
DR PROSITE; PS02079; PDGF_61; 1.
DR PROSITE; PS02078; PDGF_62; 1.
DR PROSITE; PS02079; PDGF_63; 1.
DR PROSITE; PS02078; PDGF_64; 1.
DR PROSITE; PS02079; PDGF_65; 1.
DR PROSITE; PS02078; PDGF_66; 1.
DR PROSITE; PS02079; PDGF_67; 1.
DR PROSITE; PS02078; PDGF_68; 1.
DR PROSITE; PS02079; PDGF_69; 1.
DR PROSITE; PS02078; PDGF_70; 1.
DR PROSITE; PS02079; PDGF_71; 1.
DR PROSITE; PS02078; PDGF_72; 1.
DR PROSITE; PS02079; PDGF_73; 1.
DR PROSITE; PS02078; PDGF_74; 1.
DR PROSITE; PS02079; PDGF_75; 1.
DR PROSITE; PS02078; PDGF_76; 1.
DR PROSITE; PS02079; PDGF_77; 1.
DR PROSITE; PS02078; PDGF_78; 1.
DR PROSITE; PS02079; PDGF_79; 1.
DR PROSITE; PS02078; PDGF_80; 1.
DR PROSITE; PS02079; PDGF_81; 1.
DR PROSITE; PS02078; PDGF_82; 1.
DR PROSITE; PS02079; PDGF_83; 1.
DR PROSITE; PS02078; PDGF_84; 1.
DR PROSITE; PS02079; PDGF_85; 1.
DR PROSITE; PS02078; PDGF_86; 1.
DR PROSITE; PS02079; PDGF_87; 1.
DR PROSITE; PS02078; PDGF_88; 1.
DR PROSITE; PS02079; PDGF_89; 1.
DR PROSITE; PS02078; PDGF_90; 1.
DR PROSITE; PS02079; PDGF_91; 1.
DR PROSITE; PS02078; PDGF_92; 1.
DR PROSITE; PS02079; PDGF_93; 1.
DR PROSITE; PS02078; PDGF_94; 1.
DR PROSITE; PS02079; PDGF_95; 1.
DR PROSITE; PS02078; PDGF_96; 1.
DR PROSITE; PS02079; PDGF_97; 1.
DR PROSITE; PS02078; PDGF_98; 1.
DR PROSITE; PS02079; PDGF_99; 1.
DR PROSITE; PS02078; PDGF_100; 1.
DR PROSITE; PS02079; PDGF_101; 1.
DR PROSITE; PS02078; PDGF_102; 1.
DR PROSITE; PS02079; PDGF_103; 1.
DR PROSITE; PS02078; PDGF_104; 1.
DR PROSITE; PS02079; PDGF_105; 1.
DR PROSITE; PS02078; PDGF_106; 1.
DR PROSITE; PS02079; PDGF_107; 1.
DR PROSITE; PS02078; PDGF_108; 1.
DR PROSITE; PS02079; PDGF_109; 1.
DR PROSITE; PS02078; PDGF_110; 1.
DR PROSITE; PS02079; PDGF_111; 1.
DR PROSITE; PS02078; PDGF_112; 1.
DR PROSITE; PS02079; PDGF_113; 1.
DR PROSITE; PS02078; PDGF_114; 1.
DR PROSITE; PS02079; PDGF_115; 1.
DR PROSITE; PS02078; PDGF_116; 1.
DR PROSITE; PS02079; PDGF_117; 1.
DR PROSITE; PS02078; PDGF_118; 1.
DR PROSITE; PS02079; PDGF_119; 1.
DR PROSITE; PS02078; PDGF_120; 1.
DR PROSITE; PS02079; PDGF_121; 1.
DR PROSITE; PS02078; PDGF_122; 1.
DR PROSITE; PS02079; PDGF_123; 1.
DR PROSITE; PS02078; PDGF_124; 1.
DR PROSITE; PS02079; PDGF_125; 1.
DR PROSITE; PS02078; PDGF_126; 1.
DR PROSITE; PS02079; PDGF_127; 1.
DR PROSITE; PS02078; PDGF_128; 1.
DR PROSITE; PS02079; PDGF_129; 1.
DR PROSITE; PS02078; PDGF_130; 1.
DR PROSITE; PS02079; PDGF_131; 1.
DR PROSITE; PS02078; PDGF_132; 1.
DR PROSITE; PS02079; PDGF_133; 1.
DR PROSITE; PS02078; PDGF_134; 1.
DR PROSITE; PS02079; PDGF_135; 1.
DR PROSITE; PS02078; PDGF_136; 1.
DR PROSITE; PS02079; PDGF_137; 1.
DR PROSITE; PS02078; PDGF_138; 1.
DR PROSITE; PS02079; PDGF_139; 1.
DR PROSITE; PS02078; PDGF_140; 1.
DR PROSITE; PS02079; PDGF_141; 1.
DR PROSITE; PS02078; PDGF_142; 1.
DR PROSITE; PS02079; PDGF_143; 1.
DR PROSITE; PS02078; PDGF_144; 1.
DR PROSITE; PS02079; PDGF_145; 1.
DR PROSITE; PS02078; PDGF_146; 1.
DR PROSITE; PS02079; PDGF_147; 1.
DR PROSITE; PS02078; PDGF_148; 1.
DR PROSITE; PS02079; PDGF_149; 1.
DR PROSITE; PS02078; PDGF_150; 1.
DR PROSITE; PS02079; PDGF_151; 1.
DR PROSITE; PS02078; PDGF_152; 1.
DR PROSITE; PS02079; PDGF_153; 1.
DR PROSITE; PS02078; PDGF_154; 1.
DR PROSITE; PS02079; PDGF_155; 1.
DR PROSITE; PS02078; PDGF_156; 1.
DR PROSITE; PS02079; PDGF_157; 1.
DR PROSITE; PS02078; PDGF_158; 1.
DR PROSITE; PS02079; PDGF_159; 1.
DR PROSITE; PS02078; PDGF_160; 1.
DR PROSITE; PS02079; PDGF_161; 1.
DR PROSITE; PS02078; PDGF_162; 1.
DR PROSITE; PS02079; PDGF_163; 1.
DR PROSITE; PS02078; PDGF_164; 1.
DR PROSITE; PS02079; PDGF_165; 1.
DR PROSITE; PS02078; PDGF_166; 1.
DR PROSITE; PS02079; PDGF_167; 1.
DR PROSITE; PS02078; PDGF_168; 1.
DR PROSITE; PS02079; PDGF_169; 1.
DR PROSITE; PS02078; PDGF_170; 1.
DR PROSITE; PS02079; PDGF_171; 1.
DR PROSITE; PS02078; PDGF_172; 1.
DR PROSITE; PS02079; PDGF_173; 1.
DR PROSITE; PS02078; PDGF_174; 1.
DR PROSITE; PS02079; PDGF_175; 1.
DR PROSITE; PS02078; PDGF_176; 1.
DR PROSITE; PS02079; PDGF_177; 1.
DR PROSITE; PS02078; PDGF_178; 1.
DR PROSITE; PS02079; PDGF_179; 1.
DR PROSITE; PS02078; PDGF_180; 1.
DR PROSITE; PS02079; PDGF_181; 1.
DR PROSITE; PS02078; PDGF_182; 1.
DR PROSITE; PS02079; PDGF_183; 1.
DR PROSITE; PS02078; PDGF_184; 1.
DR PROSITE; PS02079; PDGF_185; 1.
DR PROSITE; PS02078; PDGF_186; 1.
DR PROSITE; PS02079; PDGF_187; 1.
DR PROSITE; PS02078; PDGF_188; 1.
DR PROSITE; PS02079; PDGF_189; 1.
DR PROSITE; PS02078; PDGF_190; 1.
DR PROSITE; PS02079; PDGF_191; 1.
DR PROSITE; PS02078; PDGF_192; 1.
DR PROSITE; PS02079; PDGF_193; 1.
DR PROSITE; PS02078; PDGF_194; 1.
DR PROSITE; PS02079; PDGF_195; 1.
DR PROSITE; PS02078; PDGF_196; 1.
DR PROSITE; PS02079; PDGF_197; 1.
DR PROSITE; PS02078; PDGF_198; 1.
DR PROSITE; PS02079; PDGF_199; 1.
DR PROSITE; PS02078; PDGF_200; 1.
DR PROSITE; PS02079; PDGF_201; 1.
DR PROSITE; PS02078; PDGF_202; 1.
DR PROSITE; PS02079; PDGF_203; 1.
DR PROSITE; PS02078; PDGF_204; 1.
DR PROSITE; PS02079; PDGF_205; 1.
DR PROSITE; PS02078; PDGF_206; 1.
DR PROSITE; PS02079; PDGF_207; 1.
DR PROSITE; PS02078; PDGF_208; 1.
DR PROSITE; PS02079; PDGF_209; 1.
DR PROSITE; PS02078; PDGF_210; 1.
DR PROSITE; PS02079; PDGF_211; 1.
DR PROSITE; PS02078; PDGF_212; 1.
DR PROSITE; PS02079; PDGF_213; 1.
DR PROSITE; PS02078; PDGF_214; 1.
DR PROSITE; PS02079; PDGF_215; 1.
DR PROSITE; PS02078; PDGF_216; 1.
DR PROSITE; PS02079; PDGF_217; 1.
DR PROSITE; PS02078; PDGF_218; 1.
DR PROSITE; PS02079; PDGF_219; 1.
DR PROSITE; PS02078; PDGF_220; 1.
DR PROSITE; PS02079; PDGF_221; 1.
DR PROSITE; PS02078; PDGF_222; 1.
DR PROSITE; PS02079; PDGF_223; 1.
DR PROSITE; PS02078; PDGF_224; 1.
DR PROSITE; PS02079; PDGF_225; 1.
DR PROSITE; PS02078; PDGF_226; 1.
DR PROSITE; PS02079; PDGF_227; 1.
DR PROSITE; PS02078; PDGF_228; 1.
DR PROSITE; PS02079; PDGF_229; 1.
DR PROSITE; PS02078; PDGF_230; 1.
DR PROSITE; PS02079; PDGF_231; 1.
DR PROSITE; PS02078; PDGF_232; 1.
DR PROSITE; PS02079; PDGF_233; 1.
DR PROSITE; PS02078; PDGF_234; 1.
DR PROSITE; PS02079; PDGF_235; 1.
DR PROSITE; PS02078; PDGF_236; 1.
DR PROSITE; PS02079; PDGF_237; 1.
DR PROSITE; PS02078; PDGF_238; 1.
DR PROSITE; PS02079; PDGF_239; 1.
DR PROSITE; PS02078; PDGF_240; 1.
DR PROSITE; PS02079; PDGF_241; 1.
DR PROSITE; PS02078; PDGF_242; 1.
DR PROSITE; PS02079; PDGF_243; 1.
DR PROSITE; PS02078; PDGF_244; 1.
DR PROSITE; PS02079; PDGF_245; 1.
DR PROSITE; PS02078; PDGF_246; 1.
DR PROSITE; PS02079; PDGF_247; 1.
DR PROSITE; PS02078; PDGF_248; 1.
DR PROSITE; PS02079; PDGF_249; 1.
DR PROSITE; PS02078; PDGF_250; 1.
DR PROSITE; PS02079; PDGF_251; 1.
DR PROSITE; PS02078; PDGF_252; 1.
DR PROSITE; PS02079; PDGF_253; 1.
DR PROSITE; PS02078; PDGF_254; 1.
DR PROSITE; PS02079; PDGF_255; 1.
DR PROSITE; PS02078; PDGF_256; 1.
DR PROSITE; PS02079; PDGF_257; 1.
DR PROSITE; PS02078; PDGF_258; 1.
DR PROSITE; PS02079; PDGF_259; 1.
DR PROSITE; PS02078; PDGF_260; 1.
DR PROSITE; PS02079; PDGF_261; 1.
DR PROSITE; PS02078; PDGF_262; 1.
DR PROSITE; PS02079; PDGF_263; 1.
DR PROSITE; PS02078; PDGF_264; 1.
DR PROSITE; PS02079; PDGF_265; 1.
DR PROSITE; PS02078; PDGF_266; 1.
DR PROSITE; PS02079; PDGF_267; 1.
DR PROSITE; PS02078; PDGF_268; 1.
DR PROSITE; PS02079; PDGF_269; 1.
DR PROSITE; PS02078; PDGF_270; 1.
DR PROSITE; PS02079; PDGF_271; 1.
DR PROSITE; PS02078; PDGF_272; 1.
DR PROSITE; PS02079; PDGF_273; 1.
DR PROSITE; PS02078; PDGF_274; 1.
DR PROSITE; PS02079; PDGF_275; 1.
DR PROSITE; PS02078; PDGF_276; 1.
DR PROSITE; PS02079; PDGF_277; 1.
DR PROSITE; PS02078; PDGF_278; 1.
DR PROSITE; PS02079; PDGF_279; 1.
DR PROSITE; PS02078; PDGF_280; 1.
DR PROSITE; PS02079; PDGF_281; 1.
DR PROSITE; PS02078; PDGF_282; 1.
DR PROSITE; PS02079; PDGF_283; 1.
DR PROSITE; PS02078; PDGF_284; 1.
DR PROSITE; PS02079; PDGF_285; 1.
DR PROSITE; PS02078; PDGF_286; 1.
DR PROSITE; PS02079; PDGF_287; 1.
DR PROSITE; PS02078; PDGF_288; 1.
DR PROSITE; PS02079; PDGF_289; 1.
DR PROSITE; PS02078; PDGF_290; 1.
DR PROSITE; PS02079; PDGF_291; 1.
DR PROSITE; PS02078; PDGF_292; 1.
DR PROSITE; PS02079; PDGF_293; 1.
DR PROSITE; PS02078; PDGF_294; 1.
DR PROSITE; PS02079; PDGF_295; 1.
DR PROSITE; PS02078; PDGF_296; 1.
DR PROSITE; PS02079; PDGF_297; 1.
DR PROSITE; PS02078; PDGF_298; 1.
DR PROSITE; PS02079; PDGF_299; 1.
DR PROSITE; PS02078; PDGF_300; 1.
DR PROSITE; PS02079; PDGF_301; 1.
DR PROSITE; PS02078; PDGF_302; 1.
DR PROSITE; PS02079; PDGF_303; 1.
DR PROSITE; PS02078; PDGF_304; 1.
DR PROSITE; PS02079; PDGF_305; 1.
DR PROSITE; PS02078; PDGF_306; 1.
DR PROSITE; PS02079; PDGF_307; 1.
DR PROSITE; PS02078; PDGF_308; 1.
DR PROSITE; PS02079; PDGF_309; 1.
DR PROSITE; PS02078; PDGF_310; 1.
DR PROSITE; PS02079; PDGF_311; 1.
DR PROSITE; PS02078; PDGF_312; 1.
DR PROSITE; PS02079; PDGF_313; 1.
DR PROSITE; PS02078; PDGF_314; 1.
DR PROSITE; PS02079; PDGF_315; 1.
DR PROSITE; PS02078; PDGF_316; 1.
DR PROSITE; PS02079; PDGF_317; 1.
DR PROSITE; PS02078; PDGF_318; 1.
DR PROSITE; PS02079; PDGF_319; 1.
DR PROSITE; PS02078; PDGF_320; 1.
DR PROSITE; PS02079; PDGF_321; 1.
DR PROSITE; PS02078; PDGF_322; 1.
DR PROSITE; PS02079; PDGF_323; 1.
DR PROSITE; PS02078; PDGF_324; 1.
DR PROSITE; PS02079; PDGF_325; 1.
DR PROSITE; PS02078; PDGF_326; 1.
DR PROSITE; PS02079; PDGF_327; 1.
DR PROSITE; PS02078; PDGF_328; 1.
DR PROSITE; PS02079; PDGF_329; 1.
DR PROSITE; PS02078; PDGF_330; 1.
DR PROSITE; PS02079; PDGF_331; 1.
DR PROSITE; PS02078; PDGF_332; 1.
DR PROSITE; PS02079; PDGF_333; 1.
DR PROSITE; PS02078; PDGF_334; 1.
DR PROSITE; PS02079; PDGF_335; 1.
DR PROSITE; PS02078; PDGF_336; 1.
DR PROSITE; PS02079; PDGF_337; 1.
DR PROSITE; PS02078; PDGF_338; 1.
DR PROSITE; PS02079; PDGF_339; 1.
DR PROSITE; PS02078; PDGF_340; 1.
DR PROSITE; PS02079; PDGF_341; 1.
DR PROSITE; PS02078; PDGF_342; 1.
DR PROSITE; PS02079; PDGF_343; 1.
DR PROSITE; PS02078; PDGF_344; 1.
DR PROSITE; PS02079; PDGF_345; 1.
DR PROSITE; PS02078; PDGF_346; 1.
DR PROSITE; PS02079; PDGF_347; 1.
DR PROSITE; PS02078; PDGF_348; 1.
DR PROSITE; PS02079; PDGF_349; 1.
DR PROSITE; PS02078; PDGF_350; 1.
DR PROSITE; PS02079; PDGF_351; 1.
DR PROSITE; PS02078; PDGF_352; 1.
DR PROSITE; PS02079; PDGF_353; 1.
DR PROSITE; PS02078; PDGF_354; 1.
DR PROSITE; PS02079; PDGF_355; 1.
DR PROSITE; PS02078; PDGF_356; 1.
DR PROSITE; PS02079; PDGF_357; 1.
DR PROSITE; PS02078; PDGF_358; 1.
DR PROSITE; PS02079; PDGF_359; 1.
DR PROSITE; PS02078; PDGF_360; 1.
DR PROSITE; PS02079; PDGF_361; 1.
DR PROSITE; PS02078; PDGF_362; 1.
DR PROSITE; PS02079; PDGF_363; 1.
DR PROSITE; PS02078; PDGF_364; 1.
DR PROSITE; PS02079; PDGF_365; 1.
DR PROSITE; PS02078; PDGF_366; 1.
DR PROSITE; PS02079; PDGF_367; 1.
DR PROSITE; PS02078; PDGF_368; 1.
DR PROSITE; PS02079; PDGF_369; 1.
DR PROSITE; PS02078; PDGF_370; 1.
DR PROSITE; PS02079; PDGF_371; 1.
DR PROSITE; PS02078; PDGF_372; 1.
DR PROSITE; PS02079; PDGF_373; 1.
DR PROSITE; PS02078; PDGF_374; 1.
DR PROSITE; PS02079; PDGF_375; 1.
DR PROSITE; PS02078; PDGF_376; 1.
DR PROSITE; PS02079; PDGF_377; 1.
DR PROSITE; PS02078; PDGF_378; 1.
DR PROSITE; PS02079; PDGF_379; 1.
DR PROSITE; PS02078; PDGF_380; 1.
DR PROSITE; PS02079; PDGF_381; 1.
DR PROSITE; PS02078; PDGF_382; 1.
DR PROSITE; PS02079; PDGF_383; 1.
DR PROSITE; PS02078; PDGF_384; 1.
DR PROSITE; PS02079; PDGF_385; 1.
DR PROSITE; PS02078; PDGF_386; 1.
DR PROSITE; PS02079; PDGF_387; 1.
DR PROSITE; PS02078; PDGF_388; 1.
DR PROSITE; PS02079; PDGF_389; 1.
DR PROSITE; PS02078; PDGF_390; 1.
DR PROSITE; PS02079; PDGF_391; 1.
DR PROSITE; PS02078; PDGF_392; 1.
DR PROSITE; PS02079; PDGF_393; 1.
DR PROSITE; PS02078; PDGF_394; 1.
DR PROSITE; PS02079; PDGF_395; 1.
DR PROSITE; PS02078; PDGF_396; 1.
DR PROSITE; PS02079; PDGF_397; 1.
DR PROSITE; PS02078; PDGF_398; 1.
DR PROSITE; PS02079; PDGF_399; 1.
DR PROSITE; PS02078; PDGF_400; 1.
DR PROSITE; PS02079; PDGF_401; 1.
DR PROSITE; PS02078; PDGF_402; 1.
DR PROSITE; PS02079; PDGF_403; 1.
DR PROSITE; PS02078; PDGF_404; 1.
DR PROSITE; PS02079; PDGF_405; 1.
DR PROSITE; PS02078; PDGF_406; 1.
DR PROSITE; PS02079; PDGF_407; 1.
DR PROSITE; PS02078; PDGF_408; 1.
DR PROSITE; PS02079; PDGF_409; 1.
DR PROSITE; PS02078; PDGF_410; 1.
DR PROSITE; PS02079; PDGF_411; 1.
DR PROSITE; PS02078; PDGF_412; 1.
DR PROSITE; PS02079; PDGF_413; 1.
DR PROSITE; PS02078; PDGF_414; 1.
DR PROSITE; PS02079; PDGF_415; 1.
DR PROSITE; PS02078; PDGF_416; 1.
DR PROSITE; PS02079; PDGF_417; 1.
DR PROSITE; PS02078; PDGF_418; 1.
DR PROSITE; PS02079; PDGF_419; 1.
DR PROSITE; PS02078; PDGF_420; 1.
DR PROSITE; PS02079; PDGF_421; 1.
DR PROSITE; PS02078; PDGF_422; 1.
DR PROSITE; PS02079; PDGF_423; 1.
DR PROSITE; PS02078; PDGF_424; 1.
DR PROSITE; PS02079; PDGF_425; 1.
DR PROSITE; PS02078; PDGF_426; 1.
DR PROSITE; PS02079; PDGF_427; 1.
DR PROSITE; PS02078; PDGF_428; 1.
DR PROSITE; PS02079; PDGF_429; 1.
DR PROSITE; PS02078; PDGF_430; 1.
DR PROSITE; PS02079; PDGF_431; 1.
DR PROSITE; PS02078; PDGF_432; 1.
DR PROSITE; PS02079; PDGF_433; 1.
DR PROSITE; PS02078; PDGF_434; 1.
DR PROSITE; PS02079; PDGF_435; 1.
DR PROSITE; PS02078; PDGF_436; 1.
DR PROSITE; PS02079; PDGF_437; 1.
DR PROSITE; PS02078; PDGF_438; 1.
DR PROSITE; PS02079; PDGF_439; 1.
DR PROSITE; PS02078; PDGF_440; 1.
DR PROSITE; PS02079; PDGF_441; 1.
DR PROSITE; PS02078; PDGF_442; 1.
DR PROSITE; PS02079; PDGF_443; 1.
DR PROSITE; PS02078; PDGF_444; 1.
DR PROSITE; PS02079; PDGF_445; 1.
DR PROSITE; PS02078; PDGF_446; 1.
DR PROSITE; PS02079; PDGF_447; 1.
DR PROSITE; PS02078; PDGF_448; 1.
DR PROSITE; PS02079; PDGF_449; 1.
DR PROSITE; PS02078; PDGF_450; 1.
DR PROSITE; PS02079; PDGF_451; 1.
DR PROSITE; PS02078; PDGF_452; 1.
DR PROSITE; PS02079; PDGF_453; 1.
DR PROSITE; PS02078; PDGF_454; 1.
DR PROSITE; PS02079; PDGF_455; 1.
DR PROSITE; PS02078; PDGF_456; 1.
DR PROSITE; PS02079; PDGF_457; 1.
DR PROSITE; PS02078; PDGF_458; 1.
DR PROSITE; PS02079; PDGF_459; 1.
DR PROSITE; PS02078; PDGF_460; 1.
DR PROSITE; PS02079; PDGF_461; 1.
DR PROSITE; PS02078; PDGF_462; 1.
DR PROSITE; PS02079; PDGF_463; 1.
DR PROSITE; PS02078; PDGF_464; 1.
DR PROSITE; PS02079; PDGF_465; 1.
DR PROSITE; PS02078; PDGF_466; 1.
DR PROSITE; PS02079; PDGF_467; 1.
DR PROSITE; PS02078; PDGF_468; 1.
DR PROSITE; PS02079; PDGF_469; 1.
DR PROSITE; PS02078; PDGF_470; 1.
DR PROSITE; PS02079; PDGF_471; 1.
DR PROSITE; PS02078; PDGF_472; 1.
DR PROSITE; PS02079; PDGF_473; 1.
DR PROSITE; PS02078; PDGF_474; 1.
DR PROSITE; PS02079; PDGF_475; 1.
DR PROSITE; PS02078; PDGF_476; 1.
DR PROSITE; PS02079; PDGF_477; 1.
DR PROSITE; PS02078; PDGF_478; 1.
DR PROSITE; PS02079; PDGF_479; 1.
DR PROSITE; PS02078; PDGF_480; 1.
DR PROSITE; PS02079; PDGF_481; 1.
DR PROSITE; PS02078; PDGF_482; 1.
DR PROSITE; PS02079; PDGF_483; 1.
DR PROSITE; PS02078; PDGF_484; 1.
DR PROSITE; PS02079; PDGF_485; 1.
DR PROSITE; PS02078; PDGF_486; 1.
DR PROSITE; PS02079; PDGF_487; 1.
DR PROSITE; PS02078; PDGF_488; 1.
DR PROSITE; PS02079; PDGF_489; 1.
DR PROSITE; PS02078; PDGF_490; 1.
DR PROSITE; PS02079; PDGF_491; 1.
DR PROSITE; PS02078; PDGF_492; 1.
DR PROSITE; PS02079; PDGF_493; 1.
DR PROSITE; PS02078; PDGF_494; 1.
DR PROSITE; PS02079; PDGF_495; 1.
DR PROSITE; PS02078; PDGF_496; 1.
DR PROSITE; PS02079; PDGF_497; 1.
DR PROSITE; PS02078; PDGF_498; 1.
DR PROSITE; PS02079; PDGF_499; 1.
DR PROSITE; PS02078; PDGF_500; 1.
DR PROSITE; PS02079; PDGF_501; 1.
DR PROSITE; PS02078; PDGF_502; 1.
DR PROSITE; PS02079; PDGF_503; 1.
DR PROSITE; PS02078; PDGF_504; 1.
DR PROSITE; PS02079; PDGF_505; 1.
DR PROSITE; PS02078; PDGF_506; 1.
DR PROSITE; PS02079; PDGF_507; 1.
DR PROSITE; PS02078; PDGF_508; 1.
DR PROSITE; PS02079; PDGF_509; 1.
DR PROSITE; PS02078; PDGF_510; 1.
DR PROSITE; PS02079; PDGF_511; 1.
DR PROSITE; PS02078; PDGF_512; 1.
DR PROSITE; PS02079; PDGF_513; 1.
DR PROSITE; PS02078; PDGF_514; 1.
DR PROSITE; PS02079; PDGF_
```

```

CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=PI5691-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=PI5691-2; Sequence=VSP_004613, VSP_004614;
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M32976; AAA30502.1; -
DR EMBL; M31836; AAA30804.1; -
DR EMBL; M33750; AAA30805.1; -
DR PIR; A33787; A33787.
DR PIR; B40080; B40080.
DR HSP; P15692; IYGH.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF_1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT SIGNAL 1 26 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT CHAIN 27 190 BY SIMILARITY.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 82 127 BY SIMILARITY.
FT DISULFID 86 129 INTERCHAIN (BY SIMILARITY).
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (GLCNAC...) (POTENTIAL).
FT CARBOHYD 100 100 Missing (in isoform Beta).
FT VARSPLIC 139 183 /FTid=VSP_004613.
FT VARSPLIC 184 184 R -> K (in isoform Beta).
FT FTid=VSP_004614.
FT SEQUENCE 190 AA; 22310 MW; EDBF903E46E24789 CRC64;

Query Match 33.5%; Score 283.5; DB 1; Length 190;
Best Local Similarity 46.9%; Pred. No. 2.5e-22;
Matches 60; Conservative 16; Mismatches 43; Indels 9; Gaps 2;

QY 21 SQGALSAGNNSTEMEVVPFNEVWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCS 80
Db 24 SQAAPMAEGGKPHVVKFMDVQYRSCFPIETLVDIFQEYDLEIFKSCVPLMRCG 83
QY 81 GCCGDEGLHCVALKANTITMOLKIPPNRDPHVSVMFTFSODVLCCECPILETK- 135
Db 84 GCCNDESLECVPTSEFNITMIMRKPHSQH-IGEMSFLOHNCCECRPKKDKARQENPC 142
QY 136 ---AERRK 140
Db 143 GPCSERX 150

RESULT 13
VEGA_MESAU STANDARD; PRT; 190 AA.
AC Q99PS1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
GN Mesocricetus auratus (Golden hamster).
OS Mesocricetus auratus (Golden hamster).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Decidua, and Embryo;
RX MEDLINE=99311285; PubMed=10382276;
RA Yi X.-J., Jiang H.-Y., Lee K.-K., Tang P.-L., Chow P.-H.;
RT "Expression of vascular endothelial growth factor (VEGF) and its
RT receptors during embryonic implantation in the golden hamster
RT (Mesocricetus auratus).";
RL Cell Tissue Res. 296:339-349 (1999).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PLGF (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin (By
CC similarity). Belongs to the PDGF/VEGF growth factor family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
EMBL; AF063013; AAK00049.1; -
HSP; P15692; IYGH.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Multigene family.
FT SIGNAL 1 26 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT CHAIN 27 190 BY SIMILARITY.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 82 127 BY SIMILARITY.
FT DISULFID 86 129 BY SIMILARITY.
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (GLCNAC...) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 190 AA; 22276 MW; F00CSA8EA79A465F CRC64;

Query Match 33.4%; Score 282.5; DB 1; Length 190;
Best Local Similarity 46.1%; Pred. No. 3.2e-22;
Matches 59; Conservative 16; Mismatches 44; Indels 9; Gaps 2;

QY 21 SQGALSAGNNSTEMEVVPFNEVWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCS 80
Db 24 SQAAPTEGEQKAHGVVFMVYRSCFPIETLVDIFQEYDLEIFKSCVPLMRCG 83
QY 81 GCCGDEGLHCVALKANTITMOLKIPPNRDPHVSVMFTFSODVLCCECPILETK- 135
Db 84 GCCSDEALECVPTSEFNITMIMRKPHSQH-IGEMSFLOHNCCECRPKKDKARQENPC 142
QY 136 ---AERRK 140
Db 143 EPCSERX 150

```

RESULT 14
VEGA_SHEEP STANDARD; PRT; 146 AA.
AC P50412;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97117958; PubMed=8958842;
RA Redner D.A., Bai Y., Li J., Charnock-Jones D.S., Smith S.K., Reynolds L.P., Moor R.M.;
RT "Characterization and expression of vascular endothelial growth factor (VEGF) in the ovine corpus luteum.";
RL J. Reprod. Fert. 108:157-165(1996).
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PLGF (By similarity).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).
CC
CC EMBL; X89506; CAA61677.1; -.
CC PIR; S57956; S57956.
CC HSP; P15692; 1VPP.
CC InterPro; IPR002400; GF_cysknot.
CC Pfam; PF00341; PDGF; 1.
CC PRINTS; PR00438; GFCVSKNOT.
CC ProDom; PD001629; PD_growth_factor; 1.
CC SMART; SM00141; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS0278; PDGF_2; 1.
CC Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 146 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 82 127 BY SIMILARITY.
FT DISULFID 86 129 BY SIMILARITY.
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 146 AA; 17247 MW; 4E792CB557F91760 CRC64;

Query Match 33.3%; Score 282; DB 1; Length 146;
Best Local Similarity 43.9%; Pred. No. 2,7e-22;
Matches 58; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

QY 21 SQGALSAGNSTEMEVPFNEVWGRSYCRPMKLVYIADHEHNEVSHIFSPSCVLLSRCS 80
DB 24 SOAAPMAEGGQKPEHVMKFMVYQSFCHRPITLVDIFQEPDEYFKPCVFLMRCG 83

QY 81 GCGDEGLHCVALKTANITMQLKIPNRPDHFVEMTFSDVLCBCRPILETTKAERRK 140
DB 84 GCGNDESLECVPTFEFNITMQLKIPNRPDHFVEMTFSDVLCBCRPILETTKAERRK 133
QY 141 TKGKRSQSTPQ 152
DB 134 DKARQEKCDKPR 145
RESULT 15
VEGA_CAVPO STANDARD; PRT; 164 AA.
AC P26617;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor A (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bile duct;
RX Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.
RA Berse B.;
RT -!- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PLGF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).
CC
CC EMBL; M84230; AAA37057.1; -.
CC HSP; P15692; 1VGH.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR000072; PD_growth_factor.
CC Pfam; PF00341; PDGF; 1.
CC PRINTS; PR00438; GFCVSKNOT.
CC ProDom; PD001629; PD_growth_factor; 1.
CC SMART; SM00141; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS0278; PDGF_2; 1.
CC Mitogen; Angiogenesis; Growth factor; Glycoprotein.
FT DISULFID 25 67 BY SIMILARITY.
FT DISULFID 56 101 BY SIMILARITY.
FT DISULFID 60 103 BY SIMILARITY.
FT DISULFID 50 50 INTERCHAIN (BY SIMILARITY).
FT DISULFID 59 59 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 164 AA; 19330 MW; 9EB86A81A9D5DCA4 CRC64;

Query Match 33.2%; Score 280.5; DB 1; Length 164;
Best Local Similarity 50.0%; Pred. No. 4.4e-22;
Matches 57; Conservative 15; Mismatches 33; Indels 9; Gaps 2;

QY 35 EWVPNEVWGRSYCRPMKLVYIADHEHNEVSHIFSPSCVLLSRCSGCGDGLHCVALK 94
DB 12 EVVFMVDYKSYCRPMKLVYIADHEHNEVSHIFSPSCVLLSRCSGCGDGLHCVALK 71

Search completed: September 13, 2004, 09:51:24
Job time : 24 secs

Blank Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2004, 09:44:09 ; Search time 116 Seconds
(without alignments)

429.758 Million cell updates/sec

Title: US-10-071-370A-4

Perfect score: 846

Sequence: 1 MLAKLFTCFLQVLGLAVH.....RXTGKRKQSKPTQTEPHL 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp archaea:*

2: sp bacteria:*

3: sp fungi:*

4: sp human:*

5: sp invertebrate:*

6: sp mammal:*

7: sp mhc:*

8: sp organelle:*

9: sp phage:*

10: sp plant:*

11: sp rodent:*

12: sp virus:*

13: sp vertebrate:*

14: sp unclassified:*

15: sp virus:*

16: sp bacteriap:*

17: sp archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	322.5	38.1	108	Q8HY75	Q8hy75 ovis aries
2	300	35.5	189	Q95LQ4	Q95lq4 felis silve
3	299.5	35.4	190	Q91ZB1	Q91zel rattus norv
4	295.5	34.9	184	Q8HY70	Q8hy70 mustela vis
5	295	34.9	191	Q96KJ0	Q96kj0 homo sapien
6	295	34.9	191	Q96L82	Q96l82 homo sapien
7	295	34.9	191	Q95NE5	Q95ne5 macaca fasc
8	294.5	34.8	190	Q9QX39	Q9qx39 spalax leuc
9	290	34.3	126	Q9BDP7	Q9bdp7 macaca mula
10	288.5	34.1	124	Q8SPZ9	Q8spz9 sus scrofa
11	288.5	34.1	128	Q8SPL5	Q8spl5 equus cabal
12	287.5	34.0	127	Q8WMD4	Q8wmd4 sus scrofa
13	280.5	33.2	190	Q77643	Q77643 ovis aries
14	278	32.9	120	Q866G4	Q866g4 oryctolagus
15	276.5	32.7	144	Q73822	Q73822 brachydanio
16	275	32.5	118	Q9MZB1	Q9mzb1 ovis aries

ALIGNMENTS

RESULT 1

Q8HY75 Q8HY75 PRELIMINARY; PRT; 108 AA.
AC Q8HY75;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Placental growth factor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=21946003; PubMed=11945079;
RA Regnault T.R.H., Orbus R.J., de Vrijer B., Davidsen M.L., Galan H.L.,
RA Wilkening R.B., Anthony R.V.;
RT "Placental expression of VEGF, PlGF and their receptors in a model of
RT Placental insufficiency-intrauterine growth restriction (PI-IUGR).";
RL Placenta 23:132-144(2002).
DR EMBL; AY157708; AAN77495.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
FT NON_TER 1
SQ SEQUENCE 108 AA; 12634 MW; F2BC426137AC4CFC CRC64;

Query Match 38.1%; Score 322.5; DB 6; Length 108;

Best Local Similarity 56.4%; Pred. No. 1.3e-29;

Matches 57; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

Q9GK00 callithrix
O73682 brachydanio
O42572 xenopus lae
O42571 xenopus lae
Q9er16 mesocricetu
Q90x23 bothrops ja
Q90x24 bothrops ja
O70123 mus muscullu
O88911 rattus norv
Q9nl81 capreolus c
O18843 oryctolagus
Q9ymf3 orf virus.
Q9nl82 capreolus c
O97500 oryctolagus
Q809e8 orf virus.
Q80ua0 mus muscullu
Q8b571 pseudocowpo
Q8tev2 homo sapien
Q8mj86 capreolus c
Q8mi90 capra hircu
Q8mi91 capra hircu
Q91ze3 rattus norv
O57352 coturnix co
Q91zh6 meriones un
Q8qgd7 gallus gall
Q9xs50 bos taurus
Q9blx1 drosophila
Q9vwp6 drosophila

17 274.5 32.4 124 6 Q9GK00
18 273.5 32.3 188 13 O73682
19 273 32.3 194 13 O42572
20 271 32.0 148 13 O42571
21 266.5 31.5 142 11 Q9ERL6
22 264.5 30.1 146 13 Q90X23
23 254.5 30.1 146 13 Q90X24
24 229 27.1 141 11 O70123
25 225.5 26.7 110 11 O88911
26 208.5 24.6 123 6 Q9NLS1
27 207.5 24.5 75 6 O18843
28 206 24.3 132 12 Q9YMF3
29 205.5 24.3 78 6 Q9NLS2
30 200 23.6 68 6 O97500
31 191.5 22.6 136 12 Q80GE8
32 188 22.2 64 11 Q80UA0
33 180.5 21.3 152 12 Q8B571
34 178 21.0 188 4 Q8TEV2
35 158.5 18.7 131 6 Q8MJ86
36 153 18.1 65 6 Q8MIN0
37 153 18.1 326 11 Q91ZE4
38 151.5 17.9 109 6 Q8MIN1
39 144 17.0 415 11 Q91ZE3
40 144 16.5 418 13 O57352
41 140 16.5 326 11 Q91ZH6
42 137 16.2 252 13 Q8QGD7
43 134 15.8 420 6 Q9XS50
44 124.5 14.7 314 5 Q9BLX1
45 124.5 14.7 325 5 Q9VWP6

1

```

Query Match      34.9%; Score 295; DB 4; Length 191;
Best Local Similarity 47.3%; Pred. NO. 4.le-26;
Matches 61; Conservative 19; Mismatches 39; Indels 10; Gaps 3

QY 21 SQGA-LSAGNNSTMEVVPFNEVWGRSYCRPMKLVYIADSHPNVSHIFSPSCVLLSRC 79
    |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 24 SQAPMAEGGGQNHVEVKKFVDVQYSYCHPIETLVDIFQYPDBIEYIFKSPCVPLMRC 83
    |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
QY 80 SGCCGDEGLHCVALKTANITWQILKI PNROPHSVYEMTFSDVLCRPILETTK --- 135
    |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 84 GCCCNDEGLECPTFEESNITQIMRIKEHQGH-IGEMSFLOHNCRCRPFKDRARQENP 142
    |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
QY 136 ---AERRK 140
    :|||
Db 143 CGPCSERRK 151
    :|||

RESULT 6
Q96L82
ID Q96L82 PRELIMINARY; PRT; 191 AA.
AC Q96L82;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

```

[illegible]

```

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 191 AA; 22314 MW; CCE57097DD3779BD CRC64;

Query Match 34.9%; Score 295; DB 6; Length 191;
Best Local Similarity 47.9%; Pred. No. 4.1e-26;
Matches 61; Conservative 19; Mismatches 39; Indels 10; Gaps 3;

QY 21 SQGA-LSAGNSTEMEVVFNWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRC 79
Db 24 SQAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVDIFQYDEIEYIPKPSCVPLMRC 83
QY 80 SGCCGDEGLHCVALKANTITMQLIKIPNDRPHSYVEMTFSQDVLCECRPILETTK--- 135
Db 84 GGCCNDEGLECVPTESNITMQLIKPHQGH-IGEMSFLOHKNKCRPKKDRARQENP 142
QY 136 ----AERRK 140
Db 143 CGPCSERRK 151

RESULT 8
Q9QX39
ID Q9QX39 PRELIMINARY; PRT; 190 AA.
AC Q9QX39;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor.
GN VEGF.
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
OC Nanospalax.
OX NCBI_TaxID=30637;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99313148; PubMed=10386577;
RA Avivi A., Resnick M.B., Nevo E., Joel A., Levy A.P.;
RT "Adaptive hypoxic tolerance in the subterranean mole rat Spalax
RT ehrenbergi: the role of vascular endothelial growth factor.";
RL FEBS Lett. 452:133-140(1999).
DR EMBL; AF186236; AAD56245.1; -.
DR HSSP; P49763; 1FZV.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 22488 MW; 2228383BC5F0BFE CRC64;

Query Match 34.8%; Score 294.5; DB 11; Length 190;
Best Local Similarity 43.9%; Pred. No. 4.6e-26;
Matches 65; Conservative 21; Mismatches 53; Indels 9; Gaps 2;

QY 1 MLAKLFTCFQLVLAGLVHSGALSGAGNSTEMEVVFNWGRSYCRPMKLVYIADE 60
Db 4 LLSMMHWTLALILYLHAKWSQAAPTAEGEQKPHVVKFMDVFRSYCHPIETLVDIFQ 63

```

```

QY 61 HPNEVSHIFSPSCVLLSRCSCGCGDEGLHCVALKANTITMQLIKIPNDRPHSYVEMTFS 120
Db 64 YPDEIEYIPKPSCVPLMRCGGCCNDEALECVPTESNITMQLIKPHQGH-IGEMSF 122
QY 121 QDVLCECRPILETTK-----AERRK 140
Db 123 QHNRCECRPKKDRTRLENHCEPCSERRK 150

RESULT 9
Q9BDP7
ID Q9BDP7 PRELIMINARY; PRT; 126 AA.
AC Q9BDP7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
SEQUENCE FROM N.A.
RA Hazzard T.M., Nayak N.R., Jia Y., Stouffer R.L.;
RT "Rhesus macaque VEGF mRNA sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF339737; AAK26379.1; -.
DR HSSP; P49763; 1FZV.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 14599 MW; 1175F2386A883BCF CRC64;

Query Match 34.3%; Score 290; DB 6; Length 126;
Best Local Similarity 51.8%; Pred. No. 9.5e-26;
Matches 57; Conservative 16; Mismatches 35; Indels 2; Gaps 2;

QY 21 SQGA-LSAGNSTEMEVVFNWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRC 79
Db 17 SQAAHMAEGGGQNHHEVVKFMDVYQSYCHPIETLVDIFQYDEIEYIPKPSCVPLMRC 76
QY 80 SGCCGDEGLHCVALKANTITMQLIKIPNDRPHSYVEMTFSQDVLCECRP 129
Db 77 GGCCNDEGLECVPTESNITMQLIKPHQGH-IGEMSFLOHKNKCECRP 125

RESULT 10
Q8SPZ9
ID Q8SPZ9 PRELIMINARY; PRT; 124 AA.
AC Q8SPZ9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE-Myocardium;
RC TISSUE-Myocardium;
RA Yuan H., Li J.;

```

```

RT "The expression of VEGF in porcine collateral-dependent myocardial by
RT exercise training.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461807; AAL85286.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 124
FT SEQUENCE 124 AA; 14552 MW; 2E1C1A09E67C9C9 CRC64;

Query Match 34.1%; Score 288.5; DB 6; Length 124;
Best Local Similarity 50.9%; Pred. No. 1.4e-25;
Matches 58; Conservative 16; Mismatches 31; Indels 9; Gaps 2;

QY 35 EVVPFNEVWGRSVCYRPMKLVYIADEHPNEVSHIFSPSCVLLSRSCCGGDEGLHCVALK 94
Db 10 EVVKFMDVYQSRYPRIETLVDIFQEYFDEIEYIFKPSVPLMRCCGCCNDEGLECVPT 69

QY 95 TANITMQLKIPNDRPHSVEMTFSDVLCCEPILKTTK-----AERRK 140
Db 70 EFNITMQIMRIKPHQGH-IGEMSFLOHNCCECPKPKKDRARQENPCGPCSERRK 122

RESULT 11
Q8SPL5 PRELIMINARY; PRT; 128 AA.
AC Q8SPL5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN VEGF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RA Welter H., Bollwein H., Einspanier R.;
RT "Expression of horse endometrium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439887; CAD29178.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 128
FT SEQUENCE 128 AA; 14943 MW; 64EFA5DB550FC638 CRC64;

Query Match 34.1%; Score 288.5; DB 6; Length 128;
Best Local Similarity 50.9%; Pred. No. 1.4e-25;
Matches 58; Conservative 15; Mismatches 32; Indels 9; Gaps 2;

QY 35 EVVPFNEVWGRSVCYRPMKLVYIADEHPNEVSHIFSPSCVLLSRSCCGGDEGLHCVALK 94
Db 1 EVVKFMDVYQSRYPRIETLVDIFQEYFDEIEYIFKPSVPLMRCCGCCNDEGLECVPTA 60

```

```

QY 95 TANITMQLKIPNDRPHSVEMTFSDVLCCEPILKTTK-----AERRK 140
Db 61 EFNITMQIMRIKPHQGH-IGEMSFLOHNCCECPKPKKDRARQENPCGPCSERRK 113

RESULT 12
Q8WMQ4 PRELIMINARY; PRT; 127 AA.
AC Q8WMQ4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Myocardium;
RA Yuan H., Li J.;
RT "The expression of VEGF in porcine collateral-dependent myocardial by
RL exercise training.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072734; AAL68393.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 127
FT SEQUENCE 127 AA; 14920 MW; 5AB63F01AEB29ED CRC64;

Query Match 34.0%; Score 287.5; DB 6; Length 127;
Best Local Similarity 49.5%; Pred. No. 1.9e-25;
Matches 54; Conservative 18; Mismatches 36; Indels 1; Gaps 1;

QY 41 EWCGRSVCYRPMKLVYIADEHPNEVSHIFSPSCVLLSRSCCGGDEGLHCVALKNTATM 100
Db 2 DVYQSRYPRIETLVDIFQEYFDEIEYIFKPSVPLMRCCGCCNDEGLECVPTFEFNIA 61

QY 101 QILKIPNDRPHSVEMTFSDVLCCEPILKTTKAEKRTYKGRKQSK 149
Db 62 QIMRIKPHQGH-IGEMSFLOHNCCECPKPKKDRARQENPCGPCSERRK 109

RESULT 13
Q77643 PRELIMINARY; PRT; 190 AA.
AC Q77643;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor.
GN VEGF.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia-Rambouillet;
RA Cheung C.Y., Brace R.A.;
RT "Ovine vascular endothelial growth factor: Nucleotide sequence and
RT expression in fetal tissues.";

```

```

RL  Growth Factors 0:0-0(1998).
DR  EMBL: AF071015; AAC23608.1; -.
DR  HSSP; P49763; IFZV.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0008083; F:growth factor activity; IEA.
DR  GO: GO:0008151; P:cell growth and/or maintenance; IEA.
DR  InterPro: IPR002400; GF_cysknot.
DR  InterPro: IPR000072; PD_growth_factor.
DR  Pfam; PF00341; PDGF; 1.
DR  PRINTS; PR00438; GFCYSKNOT.
DR  ProDom; PD001629; PD_growth_factor; 1.
DR  SMART; SM00141; PDGF; 1.
DR  PROSITE; PS00249; PDGF_1; 1.
DR  PROSITE; PS0278; PDGF_2; 1.
DR  PROSITE; PS0278; PDGF_2; 1.
SQ  SEQUENCE 190 AA; 23542 MW; 0D5E3B3E5C53E739 CRC64;

Query Match 33.2%; Score 280.5; DB 6; Length 190;
Best Local Similarity 46.1%; Pred. No. 2e-24;
Matches 59; Conservative 17; Mismatches 43; Indels 9; Gaps 2;

QY  21 SQALSGAGNNSTEMEVVFNVEVGRSYCRPMKLVYIADHPNEVSHIFSPSCVLLSRCS 80
DB  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  24 SQAAPAEGQKQHEVYKFNVDVYQSFQPIETLVDIFQYDEIEYFKPSCVPLMRCG 83
QY  81 GCCGDEGLHCVALKTNITMQLKIPNRPDPSHYVMTFSQDVLCECRPILETWK----- 135
DB  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  84 GCCNDSELCVPTFEFNITMQLIKPHQSQH-IGEMSFLOHKNKCECRPKKQARQENPC 142
QY  136 ---AERRK 140
DB  :||||
DB  143 GPCSEERRK 150

RESULT 14
Q866G4 PRELIMINARY; PRT; 120 AA.
AC Q866G4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN VEGF.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Clausen I., Kietz S., Fischer B.;
RT "Transcriptional changes in rabbit preimplantation blastocysts upon
RT exposure to polychlorinated biphenyls.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY196796; AAC42518.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 120 AA; 14032 MW; E563C54980DCE1E8 CRC64;

Query Match 32.9%; Score 278; DB 6; Length 120;
Best Local Similarity 52.3%; Pred. No. 2.3e-24;
Matches 58; Conservative 15; Mismatches 34; Indels 4; Gaps 3;

QY  21 SQALSA--GNNSTEMEVVFNVEVGRSYCRPMKLVYIADHPNEVSHIFSPSCVLLSR 78

```

```

DB  11 SQAAPMAEEDGNKPH-EVVKFMEVYRRSYCQPIETLVDIFQYDEIEYFKPSCVPLVR 69
QY  79 CSGCGDEGLHCVALKTNITMQLKIPNRPDPSHYVMTFSQDVLCECRP 129
DB  70 CGGCCNDESLCVPTFEFNITMQLIKPHQSQH-IGEMSFLOHKNKCECRP 119

RESULT 15
O73822 PRELIMINARY; PRT; 144 AA.
AC O73822;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor 121 isoform.
GN VEGF.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Liang D., Ge R.;
RT "Vascular endothelial growth factor 121 isoform from zebrafish, Danio
RT rerio.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059661; AAC14713.1; -.
DR HSSP; P49763; IFZV.
DR ZFIN; ZDB-GENE-990415-273; vegf.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 144 AA; 16479 MW; 303E6A7407AA0832 CRC64;

Query Match 32.7%; Score 276.5; DB 13; Length 144;
Best Local Similarity 35.1%; Pred. No. 4.2e-24;
Matches 53; Conservative 35; Mismatches 54; Indels 9; Gaps 3;

QY  2 LAMKLTCTFLQVLAVHSQGLSAGNNSTEMEVVFNVEVGRSYCRPMKLVYIADHP 61
DB  3 LVVYLTLFLAALLHL SAVKAAHI PKEGKSKNDVIPFMDVYKKSACKTRELIVDIQY 62
QY  62 PNEVSHIFSPSCVLLSRCSGCCGDEGLHCVALKTNITMQLKIPNRPDPSHYVMTFSQ 121
DB  63 PDEIETHYIPSCVLMRCAGCCNDESLCVPTFEFNITMQLIKPHQSQH-QLSFTE 121
QY  122 DVLCECRPIETTKAERRKTKGRKOSKTPQ 152
DB  122 HTKCECRP-----KAE---VKAERKCEKPR 144

Search completed: September 13, 2004, 09:53:27
Job time : 118 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2004, 09:45:39 ; Search time 39 Seconds
(without alignments)
389.699 Million cell updates/sec

Title: US-10-071-370A-4
Perfect score: 846
Sequence: 1 MLAMKLFCTFLQVLAVH.....RKTGKRKQSKTPQTEPHL 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	158	2 A56125	placental growth f
2	474.5	56.1	149	2 A41236	placental growth f
3	320.5	37.9	214	2 A44881	vascular endotheli
4	315	37.2	232	2 A41551	vascular endotheli
5	300.5	35.5	190	2 B44881	vascular endotheli
6	299.5	35.4	190	2 A35987	glioma-derived vas
7	296.5	35.0	190	2 S52130	vascular endotheli
8	283.5	33.5	190	2 B40080	vascular endotheli
9	282	33.3	146	2 S57956	ovine vascular end
10	278	32.9	120	2 A33787	vascular endotheli
11	233	27.5	128	2 I51295	vascular endotheli
12	193	22.8	133	2 B49530	vascular endotheli
13	188	22.2	207	2 JC4679	vascular endotheli
14	184	21.7	188	2 JC4680	vascular endotheli
15	167	19.7	148	2 D49530	vascular endotheli
16	144	17.0	419	2 S69207	vascular endotheli
17	114	13.5	225	2 S25097	platelet-derived g
18	112	13.2	241	1 FFMGB	platelet-derived g
19	110	13.0	245	1 TVCTSS	platelet-derived g
20	108	12.8	241	1 PFHUG2	platelet-derived g
21	96.5	11.4	226	1 TVMVSS	PDGF-related trans
22	96.5	11.4	271	2 A25669	platelet-derived g
23	92.5	10.9	197	2 S25096	platelet-derived g
24	89.5	10.6	211	1 PFHUG1	platelet-derived g
25	89.5	10.6	215	2 S08220	platelet-derived g
26	84.5	10.0	196	2 A48851	platelet-derived g
27	83	9.8	226	2 I51550	spinal cord-derive
28	82.5	9.8	370	2 JC7592	platelet-derived g
29	82	9.7	370	2 JC7998	platelet-derived g

platelet-derived g
platelet-derived g
hypothetical prote
platelet-derived g
epidermal growth f
ABC transporter, p
spinal cord-derive
platelet-derived g
vitellinogen III p
hypothetical prote
protein C44E4.1a (
ribosomal protein
kinesin-related pr
conserved hypothet

30 81 9.6 166 2 JN0248
31 81 9.6 198 2 JS0735
32 81 9.6 630 2 T00351
33 80 9.5 196 2 B28964
34 78.5 9.3 1717 1 A45558
35 77.5 9.2 326 2 F81714
36 77.5 9.2 370 2 JC7591
37 77 9.1 196 2 A37359
38 77 9.1 200 2 I51551
39 77 9.1 420 2 A25876
40 76 9.0 2712 2 T30949
41 76 9.0 3864 2 D87757
42 74.5 8.8 150 2 B30097
43 74.5 8.8 153 2 A56064
44 74 8.7 701 1 B4259
45 73.5 8.7 294 2 C72050

ALIGNMENTS

RESULT 1

A56125
Placental growth factor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C;Accession: A56125
R;Disalvo, J.; Bayne, M.L.; Conn, G.; Kwok, P.W.; Trivedi, P.G.; Soderman, D.D.; Palisi,
J. Biol. Chem. 270, 7717-7723, 1995
A;Title: Purification and characterization of a naturally occurring vascular endothelial
A;Reference number: A56125; MUID:95221439; PMID:7706320
A;Accession: A56125
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-158 <DIS>
A;Cross-references: GB:L40030; NID:gl263413; PIDN:AAA97426.1; PID:gl263414
C;Keywords: glycoprotein

Query Match 100.0%; Score 846; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 4.4e-78;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAMKLFCTFLQVLAVHSGALSGNNSTEMEVFNEVWGSRCPMEKLYIAD 60
DB 1 MLAMKLFCTFLQVLAVHSGALSGNNSTEMEVFNEVWGSRCPMEKLYIAD 60
QY 61 HPNEVSHIFSPCVLLSCGCGDEGLHCVALKTANITMQLKTPPNRDPHSYVEMTFS 120
DB 61 HPNEVSHIFSPCVLLSCGCGCGDEGLHCVALKTANITMQLKTPPNRDPHSYVEMTFS 120
QY 121 QDVLCECRPILETTKAERKTKGKRKQSKTPQTEPHL 158
DB 121 QDVLCECRPILETTKAERKTKGKRKQSKTPQTEPHL 158

RESULT 2

A41236
Placental growth factor precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 05-Nov-1999
C;Accession: A41236
R;Maglione, D.; Guerriero, V.; Viglietto, G.; Delli-Bovi, P.; Persico, M.G.
Proc. Natl. Acad. Sci. U.S.A. 88, 9267-9271, 1991
A;Title: Isolation of a human placenta cDNA coding for a protein related to the vascular
A;Reference number: A41236; MUID:92021031; PMID:1924389
A;Accession: A41236
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <MAG>
A;Cross-references: GB:X54936; NID:g35521; PIDN:CAA38698.1; PID:g35522
C;Genetics:
A;Gene: GDB:PGF
A;Cross-references: GDB:I34676; OMIM:601121

[illegible]

FOIA b 7 - D

Fri Sep 17 12:13:00 2004

C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein; mit

Query Match 35.5%; Score 300.5; DB 2; Length 190;
Best Local Similarity 47.7%; Pred. No. 6.9e-23;
Matches 61; Conservative 18; Mismatches 40; Indels 9; Gaps 2;

QY 21 SQGALSAGNNSTEMEVVFNWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCS 80
DB 24 SQAAPTTEGEQKSHVEIKFMDVIQSRYPETLVDIFQYDPDEIYIFKPSCVPLMRCA 83

QY 81 GCCGDEGLHCVALKANTITMQLKIPNDRPHSYVEMTFSQDVLCECRPILETTK----- 135
DB 84 GCCNDEALECVPTSESNTITMQLRIKPHQSQH-IGEMSFLOHSRCECRPKKDRTPENHC 142

QY 136 ---AERRK 140
DB 143 EPCSERRK 150

RESULT 6
A35987
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C;Accession: A35987
R;Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Hope,
Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is ho
A;Reference number: A35987; MUID:90207249; PMID:2320579
A;Accession: A35987
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <CON>
A;Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288

Query Match 35.4%; Score 299.5; DB 2; Length 190;
Best Local Similarity 47.7%; Pred. No. 8.7e-23;
Matches 61; Conservative 18; Mismatches 40; Indels 9; Gaps 2;

QY 21 SQGALSAGNNSTEMEVVFNWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCS 80
DB 24 SQAAPTTEGEQKSHVEIKFMDVIQSRYPETLVDIFQYDPDEIYIFKPSCVPLMRCA 83

QY 81 GCCGDEGLHCVALKANTITMQLKIPNDRPHSYVEMTFSQDVLCECRPILETTK----- 135
DB 84 GCCNDEALECVPTSESNTITMQLRIKPHQSQH-IGEMSFLOHSRCECRPKKDRTPENHC 142

QY 136 ---AERRK 140
DB 143 EPCSERRK 150

RESULT 7
S52130
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S52130
R;Sharma, H.S.; Tang, Z.H.; Cho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A;Title: Nucleotide sequence and expression of the porcine vascular endothelial growth f
A;Reference number: S52130; MUID:95143284; PMID:7841203
A;Accession: S52130
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <SHA>
A;Cross-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560

Query Match 35.0%; Score 296.5; DB 2; Length 190;
Best Local Similarity 48.4%; Pred. No. 1.8e-22;
Matches 62; Conservative 17; Mismatches 40; Indels 9; Gaps 2;

QY 21 SQGALSAGNNSTEMEVVFNWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCS 80

C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein; mit

Query Match 37.2%; Score 315; DB 2; Length 232;
Best Local Similarity 47.7%; Pred. No. 2.9e-24;
Matches 62; Conservative 21; Mismatches 45; Indels 2; Gaps 2;

QY 21 SQGALSAGNNSTEMEVVFNWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCS 79
DB 24 SQAAPMAGGGONHVEVVKFMDVIQSRYPETLVDIFQYDPDEIYIFKPSCVPLMRCS 83

QY 80 SGGCGDEGLHCVALKANTITMQLKIPNDRPHSYVEMTFSQDVLCECRPILETTKERR 139
DB 84 GCCNDEALECVPTSESNTITMQLRIKPHQSQH-IGEMSFLOHNCRCRPKKDRAROEKK 142

QY 140 KTKGKRQSK 149
DB 143 SVRGKGRGQK 152

RESULT 5
B44881
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
C;Accession: B44881; A43351; A61029
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A;Reference number: A44881; MUID:92274860; PMID:1592003
A;Accession: B44881
A;Molecule type: mRNA
A;Residues: 1-190 <BRE>
A;Cross-references: GB:S38083; NID:g249858; PIDN:AAB22253.1; PID:g249859
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBI:107623)
R;Claffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
A;Title: Vascular endothelial growth factor. Regulation by cell differentiation and acti
A;Reference number: A43351; MUID:92355593; PMID:1644816
A;Accession: A43351
A;Molecule type: mRNA
A;Residues: 1-116, 'ER', 119-190 <CLA>
A;Cross-references: GB:M95200; NID:g202350; PIDN:AAA40547.1; PID:g202351
A;Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBI:110675)
R;Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.
Growth Factors 4, 53-59, 1990
A;Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial
A;Reference number: A61029; MUID:91197543; PMID:2085441
A;Accession: A61029
A;Molecule type: protein
A;Residues: 27-38 <ROS>

Db 24 SQAAPMAEGGQKPEHVMFMDVYQSFRCPIETLVDIFQYDEIEYIFKSCVPLMRG 83
 QY 81 GCCGDEGLHCVALKTANTIMQILKIPNDRPHSYVEMTFSDVLCCECPILETTK-----135
 Db 84 GCCNDESELCVPTTEFNITMQIMRIKPHQSOH-IGEMSFLOHNCCECRPKDRAQENPC 142
 QY 136 ---AERRK 140
 Db 143 GPCSERK 150

RESULT 8
 B40080
 vascular endothelial growth factor precursor (version 2) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
 C:Accession: B40080; B33787; A33255
 R:Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
 Science 246, 1306-1309, 1989
 A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
 A:Reference number: A40080; MUID:90069608; PMID:2479986
 A:Accession: B40080
 A:Molecule type: mRNA
 A:Residues: 1-190 <LEU>

A:Cross-references: GB:M32976; NID:G163006; PIDN:AAA30502.1; PID:G163007
 R:Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crispien
 Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
 A:Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
 A:Reference number: A33787; MUID:90121225; PMID:2610687
 A:Accession: B33787
 A:Molecule type: mRNA
 A:Residues: 27-190 <TIS>
 A:Cross-references: GB:M31836; NID:G163808; PIDN:AAA30804.1; PID:G163809
 R:Ferrara, N.; Henzel, W.J.
 Biochem. Biophys. Res. Commun. 161, 851-858, 1989
 A:Title: Pituitary follicular cells secrete a novel heparin-binding growth factor specific
 A:Reference number: A33255; MUID:89286596; PMID:2735925
 A:Accession: A33255
 A:Molecule type: protein

A:Residues: 27-31 <PER>
 C:Keywords: alternative splicing; glycoprotein
 F1-26/Domain: signal sequence #status predicted <SIG>
 F127-190/Product: vascular endothelial growth factor #status predicted <MAT>
 F100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.5%; Score 283.5; DB 2; Length 190;
 Best Local Similarity 46.9%; Pred. No. 3.6e-21;
 Matches 60; Conservative 16; Mismatches 43; Indels 9; Gaps 2;
 QY 21 SQGALSAGNNSTEMEVVPFNEVWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCS 80
 Db 24 SQAAPMAEGGQKPEHVMFMDVYQSFRCPIETLVDIFQYDEIEYIFKSCVPLMRG 83
 QY 81 GCCGDEGLHCVALKTANTIMQILKIPNDRPHSYVEMTFSDVLCCECPILETTK-----135
 Db 84 GCCNDESELCVPTTEFNITMQIMRIKPHQSOH-IGEMSFLOHNCCECRPKDRAQENPC 142
 QY 136 ---AERRK 140
 Db 143 GPCSERK 150

RESULT 9
 S57956
 ovine vascular endothelial growth factor - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
 C:Accession: S57956
 R:Redmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M.
 submitted to the EMBL Data Library, July 1995
 A:Reference number: S57956
 A:Accession: S57956

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-146 <RNA>
 A:Cross-references: ENBL:X89506; NID:9899350; PIDN:CAA61677.1; PID:9899351

Query Match 33.3%; Score 282; DB 2; Length 146;
 Best Local Similarity 43.9%; Pred. No. 3.9e-21;
 Matches 58; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

QY 21 SQGALSAGNNSTEMEVVPFNEVWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCS 80
 Db 24 SQAAPMAEGGQKPEHVMFMDVYQSFRCPIETLVDIFQYDEIEYIFKSCVPLMRG 83
 QY 81 GCCGDEGLHCVALKTANTIMQILKIPNDRPHSYVEMTFSDVLCCECPILETTKAERRK 140
 Db 84 GCCNDESELCVPTTEFNITMQIMRIKPHQSOH-IGEMSFLOHNCCECRP-----KK 133
 QY 141 TKGRKQSKTPQ 152
 Db 134 DKARQEKCDKPR 145

RESULT 10

A33787
 vascular endothelial growth factor (version 1) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999
 C:Accession: A33787
 R:Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crispien
 Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
 A:Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
 A:Reference number: A33787; MUID:90121225; PMID:2610687
 A:Accession: A33787
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-120 <TIS>
 A:Cross-references: GB:M33750; NID:G163810; PIDN:AAA30805.1; PID:G163811
 C:Keywords: alternative splicing

Query Match 32.9%; Score 278; DB 2; Length 120;
 Best Local Similarity 46.6%; Pred. No. 7.9e-21;
 Matches 55; Conservative 19; Mismatches 34; Indels 10; Gaps 2;
 QY 35 EYVPFNEVWGRSYCRPMKLVYIADEHPNEVSHIFSPSCVLLSRCSGCCGDEGLHCVALK 94
 Db 12 EVVKFMDVYQSFRCPIETLVDIFQYDEIEYIFKSCVPLMRGCGCNDSELCVPTTE 71
 QY 95 TANITMQILKIPNDRPHSYVEMTFSDVLCCECPILETTKAERRKTKGRKQSKTPQ 152
 Db 72 EFNITMQIMRIKPHQSOH-IGEMSFLOHNCCECRP-----KKDKARQEKCDKPR 119

RESULT 11

I51295
 vascular endothelial growth factor - quail (fragment)
 C:Species: Phasianidae gen. sp. (quail)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Feb-1997
 C:Accession: I51295
 R:Flamme, I.; Breiter, G.; Risau, W.
 Dev. Biol. 169, 699-712, 1995
 A:Title: Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1) are expressed
 A:Reference number: I51295; MUID:95301109; PMID:7781909
 A:Accession: I51295
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-128 <FLA>
 A:Cross-references: GB:S78343; NID:9999147; PID:9999148
 C:Genetics:
 A:Gene: VEGF

Query Match 27.5%; Score 233; DB 2; Length 128;
 Best Local Similarity 42.9%; Pred. No. 3e-16;
 Matches 45; Conservative 21; Mismatches 33; Indels 6; Gaps 2;

QY 57 IADHPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTANITMOILKIPPNRDPHSYVE 116
 Db 2 IFQEIYDEVEIIFRSPCVLMRCAGCGDEGLHCVALKTANITMOILKIPPNRDPHSYVE 60
 QY 117 MTFSDVLCRPILET-----TKAERRKTGKRKQSKTPQTEEP 156
 Db 61 MSFLQHSKDCRPPKGVKNQKESKRGKGGKQKRRKKGRIKPP 105
 RESULT 12
 B49530
 vascular endothelial growth factor homolog A2R, 14.7K - Orf virus
 C:Species: Orf virus
 C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C:Accession: B49530
 R:Lyttille, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
 J. Virol. 68, 84-92, 1994
 A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus orf
 A:Reference number: A49530; MUID:94076465; PMID:8254780
 A:Contents: N22
 A:Accession: B49530
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-133 <LYT>
 A:Cross-references: GB:S67520; NID:g456897; PIDN:AAB29220.1; PID:g456899
 A:Note: sequence inconsistent with nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:141420, NCBIPI:141425)
 Query Match 22.8%; Score 193; DB 2; Length 133;
 Best Local Similarity 31.5%; Pred. No. 3.4e-12;
 Matches 45; Conservative 27; Mismatches 61; Indels 10; Gaps 4;
 QY 4 MKLFTCFLOVLAVHSGQALSGAGNNSTEMEVVFPNEVWGRSYCRPMKLVYIADEPN 63
 Db 1 MKL---LVGILVAVCLH-QYLLNADSNK-----GWSEVLKSGECKPRPIVVPVSETHPE 51
 QY 64 EVSHIFSPSCVLLSRSCGCGDEGLHCVALKTANITMOILKIPPNRDPHSYVEVTFSDV 123
 Db 52 LTSQRFNPPCVLMRCGCGCNDESLECVPTTEVNTMELLG-ASGSGSGMGQRLSFVEHK 110
 QY 124 LCECRPILETTKAERRKTGKRK 146
 Db 111 KDCRPRFTTPTTPTRPRRRR 133
 RESULT 13
 Jc4679
 vascular endothelial growth factor-related factor 186 precursor - mouse
 N:Alternate names: VRF 186 protein, VEGF 186
 C:Species: Mus musculus (house mouse)
 C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
 C:Accession: Jc4679
 R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjold, M.; Weber, G.;
 Biochem. Biophys. Res. Commun. 220, 922-928, 1996
 A:Title: Characterization of the murine VEGF-related factor gene.
 A:Reference number: Jc4679; MUID:96183052; PMID:8607868
 A:Accession: Jc4679
 A:Molecule type: mRNA
 A:Residues: 1-207 <TOW>
 A:Cross-references: GB:U43836; NID:g1703480; PIDN:AAC52932.1; PID:g1314334
 C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belong
 lar endothelial growth factors 167 and 186.
 C:Genetics:
 A:Gene: vrf
 A:Map position: 19
 C:Keywords: growth factor
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-207/Product: vascular endothelial growth factor related factor #status predicted <M
 Query Match 22.2%; Score 188; DB 2; Length 207;
 Best Local Similarity 33.1%; Pred. No. 1.8e-11;
 Matches 53; Conservative 22; Mismatches 61; Indels 24; Gaps 5;

QY 1 MLAMKLTFCFLOVLAVHSGQALSGAGNNSTEMEVVFPNEVWGRSYCRPMKLVYIADE 60
 Db 4 LLRRLLVALLQARTQAPVSO----FDGFSHOKKVPVMDIVYARATCQPREVVVPLSME 59
 QY 61 HPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTANITMOILKIPPNRDPHSYV-EMTF 119
 Db 60 LMGNVVKQLVPSCVTVQRCGCCPDGGLCEVPTGQHQRVQMILMI----QYFSSQLGEMSL 116
 QY 120 SQDVLCECRPILETTKAERRKTGKRKQS--KTFQTEEPH 157
 Db 117 EEHSQCECRP-----KKESAVKPDORVAIPH 142
 RESULT 14
 Jc4680
 vascular endothelial growth factor-related factor 167 precursor - mouse
 N:Alternate names: VRF 167 protein
 C:Species: Mus musculus (house mouse)
 C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
 C:Accession: Jc4680
 R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjold, M.; Weber, G.;
 Biochem. Biophys. Res. Commun. 220, 922-928, 1996
 A:Title: Characterization of the murine VEGF-related factor gene.
 A:Reference number: Jc4679; MUID:96183052; PMID:8607868
 A:Accession: Jc4680
 A:Molecule type: mRNA
 A:Residues: 1-188 <TOW>
 A:Cross-references: GB:U43837; NID:g1314335; PIDN:AAC52553.1; PID:g1314336
 C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belong
 ar endothelial growth factors 167 and VEGF 186.
 C:Genetics:
 A:Gene: vrf
 A:Map position: 19
 A:Introns: 137/2
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-188/Product: vascular endothelial growth factor-related factor #status predicted <M
 Query Match 21.7%; Score 184; DB 2; Length 188;
 Best Local Similarity 33.6%; Pred. No. 4e-11;
 Matches 50; Conservative 21; Mismatches 56; Indels 22; Gaps 4;
 QY 1 MLAMKLTFCFLOVLAVHSGQALSGAGNNSTEMEVVFPNEVWGRSYCRPMKLVYIADE 60
 Db 4 LLRRLLVALLQARTQAPVSO----FDGFSHOKKVPVMDIVYARATCQPREVVVPLSME 59
 QY 61 HPNEVSHIFSPSCVLLSRSCGCGDEGLHCVALKTANITMOILKIPPNRDPHSYV-EMTF 119
 Db 60 LMGNVVKQLVPSCVTVQRCGCCPDGGLCEVPTGQHQRVQMILMI----QYFSSQLGEMSL 116
 QY 120 SQDVLCECRPILETTKAERRKTGKRKQS 148
 Db 117 EEHSQCECRP-----KKES 131
 RESULT 15
 D49530
 16K vascular endothelial growth factor homolog A2R - Orf virus
 C:Species: Orf virus
 C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C:Accession: D49530
 R:Lyttille, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
 J. Virol. 68, 84-92, 1994
 A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus orf
 A:Reference number: A49530; MUID:94076465; PMID:8254780
 A:Contents: N27
 A:Accession: D49530
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-148 <LYT>
 A:Cross-references: GB:S67522; NID:g456900; PIDN:AAB29223.1; PID:g456902
 A:Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBIPI:141426)

```

Query Match      19.7%; Score 167; DB 2; Length 148;
Best Local Similarity 28.1%; Pred. No. 1.6e-09;
Matches 43; Conservative 31; Mismatches 59; Indels 20; Gaps 6;

QY 4 MKLFTCLQVLGLAV---HSQGLSAGNNSTEMEVVPEFNEVWGR-----SYCRPMEKIVY 56
Db 1 MKL-TATLQVVVALLICWYNLPECVQSQNDSP-----PSTNDWMTLTKSCCKPRDTVVY 54

QY 57 IADEHPNEVSHIFSPSCVLLSRCSGCCGDEGLHCVALKTAN--ITMQILKIPPNRDPHSY 114
Db 55 LGEEYPESTNLQYNPRCVTVKRCSCGCCNGDQICTAVETRTTIVTSVTVGVSSSSGTSNG 114

QY 115 V-----EMTFSQDVLCECRPILETTKAERRTK 142
Db 115 VSTNLQRISVTEHTKCDICGRTTTTPTTTREPR 147

```

Search completed: September 13, 2004, 09:54:11
Job time : 40 secs